

=> file medline

FILE 'MEDLINE' ENTERED AT 12:07:23 ON 28 JUL 2003

FILE LAST UPDATED: 26 JUL 2003 (20030726/UP). FILE COVERS 1958 TO DATE.

On April 13, 2003, MEDLINE was reloaded. See HELP RLOAD for details.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2003 vocabulary. See <http://www.nlm.nih.gov/mesh/changes2003.html> for a description on changes.

This file contains CAS Registry Numbers for easy and accurate substance identification.

CT = controlled terminology
 NT = narrower term
 BI = Biosynthesis
 IP = isolation & purification
 2 cites

=> d que 149

L43 37021 SEA FILE=MEDLINE ABB=ON PLU=ON CAROTENOIDS+NT/CT
 L44 82158 SEA FILE=MEDLINE ABB=ON PLU=ON OXYGEN/CT
 L47 1414 SEA FILE=MEDLINE ABB=ON PLU=ON L43(L)(BI OR IP)/CT
 L48 41 SEA FILE=MEDLINE ABB=ON PLU=ON L47 AND L44
 L49 2 SEA FILE=MEDLINE ABB=ON PLU=ON L48 AND (BIOGENESIS OR GIGANTEUS)/TI

=> file caba

FILE 'CABA' ENTERED AT 12:07:25 ON 28 JUL 2003
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FILE COVERS 1973 TO 7 Jul 2003 (20030707/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> d que 167

L63 15147 SEA FILE=CABA ABB=ON PLU=ON CAROTEN?
 L64 884 SEA FILE=CABA ABB=ON PLU=ON L63 AND (CULTUR? OR FERMENT?)
 L65 8723 SEA FILE=CABA ABB=ON PLU=ON (OXYGEN? OR AEROB? OR O2 OR AERAT?)(5A)(VARY? OR CONTROL? OR LEVEL OR UPTAK? OR CONCENTRAT? OR AMOUNT)
 L66 7 SEA FILE=CABA ABB=ON PLU=ON L64 AND L65
 L67 1 SEA FILE=CABA ABB=ON PLU=ON L66 AND SUCCINATE/TI

=> file biotechno

FILE 'BIOTECHNO' ENTERED AT 12:07:26 ON 28 JUL 2003
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FILE LAST UPDATED: 22 JUL 2003 <20030722/UP>
 FILE COVERS 1980 TO DATE.

>>> SIMULTANEOUS LEFT AND RIGHT TRUNCATION AVAILABLE IN
 /CT AND BASIC INDEX <<<

=> d que 158

L53 2639 SEA FILE=BIOTECHNO ABB=ON PLU=ON ?CAROTEN?
 L54 393 SEA FILE=BIOTECHNO ABB=ON PLU=ON L53 AND (CULTUR? OR

FERMENT?)
 L55 73 SEA FILE=BIOTECHNO ABB=ON PLU=ON L54 AND (OXYGEN? OR AEROB?
 OR O2 OR AERAT?)
 L56 4620 SEA FILE=BIOTECHNO ABB=ON PLU=ON (OXYGEN? OR AEROB? OR O2 OR
 AERAT?)(5A)(VARY? OR CONTROL? OR CONCENTRAT? OR AMOUNT).
 L57 10 SEA FILE=BIOTECHNO ABB=ON PLU=ON L55 AND L56
 L58 3 SEA FILE=BIOTECHNO ABB=ON PLU=ON L57 AND (FOAM OR STOICHIOMET 3 cites
 RIC OR GLUT?)/TI

=> file hcaplus

FILE 'HCAPLUS' ENTERED AT 12:07:28 ON 28 JUL 2003
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FILE COVERS 1907 - 28 Jul 2003 VOL 139 ISS 5
 FILE LAST UPDATED: 27 Jul 2003 (20030727/ED)



This file contains CAS Registry Numbers for easy and accurate substance identification.

=> d que 118

L5 42 SEA FILE=REGISTRY ABB=ON PLU=ON (472-61-7/BI OR 4418-73-9/BI
 OR 144-68-3/BI OR 432-68-8/BI OR 4339-77-9/BI OR 4418-72-8/BI
 OR 514-78-3/BI OR 7235-40-7/BI OR 472-70-8/BI OR 108-20-3/BI
 OR 108-88-3/BI OR 108-94-1/BI OR 109-99-9/BI OR 110-54-3/BI OR
 110-82-7/BI OR 110-86-1/BI OR 116-30-3/BI OR 123-86-4/BI OR
 123-91-1/BI OR 1330-20-7/BI OR 141-78-6/BI OR 142-82-5/BI OR
 162875-45-8/BI OR 19866-02-5/BI OR 222713-29-3/BI OR 334071-56-
 6/BI OR 382660-64-2/BI OR 382660-65-3/BI OR 432-70-2/BI OR
 472-93-5/BI OR 502-65-8/BI OR 563-80-4/BI OR 60-29-7/BI OR
 64-17-5/BI OR 67-56-1/BI OR 67-64-1/BI OR 67-66-3/BI OR
 71-23-8/BI OR 71-43-2/BI OR 75-09-2/BI OR 7782-44-7/BI OR
 78-93-3/BI)
 L8 18 SEA FILE=REGISTRY ABB=ON PLU=ON L5 AND C6/ES
 L9 15 SEA FILE=REGISTRY ABB=ON PLU=ON L8 NOT 46.150.18/RID
 L10 1 SEA FILE=REGISTRY ABB=ON PLU=ON 7782-44-7
 L11 32232 SEA FILE=HCAPLUS ABB=ON PLU=ON CAROTENES+PFT,NT/CT
 L12 66957 SEA FILE=HCAPLUS ABB=ON PLU=ON L9
 L13 7229 SEA FILE=HCAPLUS ABB=ON PLU=ON (L11 OR L12)(L)PREP/RL
 L14 78324 SEA FILE=HCAPLUS ABB=ON PLU=ON FERMENTATION+PFT/CT
 L15 8976 SEA FILE=HCAPLUS ABB=ON PLU=ON CULTURE MEDIA +PFT/CT
 L16 373 SEA FILE=HCAPLUS ABB=ON PLU=ON L13 AND (L14 OR L15)
 L17 317219 SEA FILE=HCAPLUS ABB=ON PLU=ON L10
 L18 7 SEA FILE=HCAPLUS ABB=ON PLU=ON L16 AND L17 7 cites

*all carotenoids
in appl's citec*

*all of the
cpds indexed
in the cite
for applicants
priority docu-
ment*

*want cpds w/  ring
no  rings*

*PFT = old, new;
"used for" terms
preparative role*

=> d que 122

L5 42 SEA FILE=REGISTRY ABB=ON PLU=ON (472-61-7/BI OR 4418-73-9/BI OR 144-68-3/BI OR 432-68-8/BI OR 4339-77-9/BI OR 4418-72-8/BI OR 514-78-3/BI OR 7235-40-7/BI OR 472-70-8/BI OR 108-20-3/BI OR 108-88-3/BI OR 108-94-1/BI OR 109-99-9/BI OR 110-54-3/BI OR 110-82-7/BI OR 110-86-1/BI OR 116-30-3/BI OR 123-86-4/BI OR 123-91-1/BI OR 1330-20-7/BI OR 141-78-6/BI OR 142-82-5/BI OR 162875-45-8/BI OR 19866-02-5/BI OR 222713-29-3/BI OR 334071-56-6/BI OR 382660-64-2/BI OR 382660-65-3/BI OR 432-70-2/BI OR 472-93-5/BI OR 502-65-8/BI OR 563-80-4/BI OR 60-29-7/BI OR 64-17-5/BI OR 67-56-1/BI OR 67-64-1/BI OR 67-66-3/BI OR 71-23-8/BI OR 71-43-2/BI OR 75-09-2/BI OR 7782-44-7/BI OR 78-93-3/BI)

L8 18 SEA FILE=REGISTRY ABB=ON PLU=ON L5 AND C6/ES

L9 15 SEA FILE=REGISTRY ABB=ON PLU=ON L8 NOT 46.150.18/RID

L11 32232 SEA FILE=HCAPLUS ABB=ON PLU=ON CAROTENES+PFT,NT/CT

L12 66957 SEA FILE=HCAPLUS ABB=ON PLU=ON L9

L13 7229 SEA FILE=HCAPLUS ABB=ON PLU=ON (L11 OR L12)(L)PREP/RL

L14 78324 SEA FILE=HCAPLUS ABB=ON PLU=ON FERMENTATION+PFT/CT

L15 8976 SEA FILE=HCAPLUS ABB=ON PLU=ON CULTURE MEDIA +PFT/CT

L16 373 SEA FILE=HCAPLUS ABB=ON PLU=ON L13 AND (L14 OR L15)

L19 2187 SEA FILE=HCAPLUS ABB=ON PLU=ON BUBBLING/CT

L20 1915 SEA FILE=HCAPLUS ABB=ON PLU=ON AERATION/CT

L21 365 SEA FILE=HCAPLUS ABB=ON PLU=ON AERATORS/CT

L22 3 SEA FILE=HCAPLUS ABB=ON PLU=ON L16 AND (L19 OR L20 OR L21) 3 cites

=> s 118 or 122

L79 8 L18 OR L22 8 cites total for HCAPLUS

=> file wpix

FILE 'WPIX' ENTERED AT 12:07:30 ON 28 JUL 2003
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FILE LAST UPDATED: 23 JUL 2003 <20030723/UP>
 MOST RECENT DERWENT UPDATE: 200347 <200347/DW>
 DERWENT WORLD PATENTS INDEX SUBSCRIBER FILE, COVERS 1963 TO DATE

>>> NEW WEEKLY SDI FREQUENCY AVAILABLE --> see NEWS <<<

>>> SLART (Simultaneous Left and Right Truncation) is now available in the /ABEX field. An additional search field /BIX is also provided which comprises both /BI and /ABEX <<<

>>> PATENT IMAGES AVAILABLE FOR PRINT AND DISPLAY <<<

>>> FOR DETAILS OF THE PATENTS COVERED IN CURRENT UPDATES,
 SEE <http://www.derwent.com/dwpi/updates/dwpicov/index.html> <<<

>>> FOR A COPY OF THE DERWENT WORLD PATENTS INDEX STN USER GUIDE,
 PLEASE VISIT:
http://www.stn-international.de/training_center/patents/stn_guide.pdf <<<

>>> FOR INFORMATION ON ALL DERWENT WORLD PATENTS INDEX USER
 GUIDES, PLEASE VISIT:

http://www.derwent.com/userguides/dwpi_guide.html <<<

=> d que 133

| | | | | | |
|-----|-------|----------------------|--------|--|---------|
| L24 | 3123 | SEA FILE=WPIX ABB=ON | PLU=ON | ?CAROTEN? | |
| L25 | 40704 | SEA FILE=WPIX ABB=ON | PLU=ON | ?FERMENT? | |
| L26 | 1546 | SEA FILE=WPIX ABB=ON | PLU=ON | CULTUR? MEDIA | |
| L27 | 37669 | SEA FILE=WPIX ABB=ON | PLU=ON | MICROB? | |
| L28 | 236 | SEA FILE=WPIX ABB=ON | PLU=ON | L24 AND (L25 OR L26 OR L27) | |
| L29 | 15 | SEA FILE=WPIX ABB=ON | PLU=ON | L28 AND OXYGEN | |
| L30 | 1 | SEA FILE=WPIX ABB=ON | PLU=ON | L28 AND O2 | |
| L31 | 16 | SEA FILE=WPIX ABB=ON | PLU=ON | (L29 OR L30) | |
| L32 | 11 | SEA FILE=WPIX ABB=ON | PLU=ON | L31 NOT (SKIN OR DOUGH OR EMBDEN-MEYERHOF)/TI | |
| L33 | 4 | SEA FILE=WPIX ABB=ON | PLU=ON | L32 AND (CANTHAXANTHIN OR CHEMICALLY DEFINED OR NUTRIENT OR CONCENTRATES)/TI | 4 cites |

=> d que 140

| | | | | | |
|-----|-------|----------------------|--------|-------------------------------------|--------|
| L24 | 3123 | SEA FILE=WPIX ABB=ON | PLU=ON | ?CAROTEN? | |
| L25 | 40704 | SEA FILE=WPIX ABB=ON | PLU=ON | ?FERMENT? | |
| L26 | 1546 | SEA FILE=WPIX ABB=ON | PLU=ON | CULTUR? MEDIA | |
| L27 | 37669 | SEA FILE=WPIX ABB=ON | PLU=ON | MICROB? | |
| L28 | 236 | SEA FILE=WPIX ABB=ON | PLU=ON | L24 AND (L25 OR L26 OR L27) | |
| L29 | 15 | SEA FILE=WPIX ABB=ON | PLU=ON | L28 AND OXYGEN | |
| L30 | 1 | SEA FILE=WPIX ABB=ON | PLU=ON | L28 AND O2 | |
| L31 | 16 | SEA FILE=WPIX ABB=ON | PLU=ON | (L29 OR L30) | |
| L36 | 685 | SEA FILE=WPIX ABB=ON | PLU=ON | L24(5A)(PRODUC? OR PREP?) | |
| L37 | 46 | SEA FILE=WPIX ABB=ON | PLU=ON | L36 AND OXYGEN? | |
| L38 | 19 | SEA FILE=WPIX ABB=ON | PLU=ON | L37 AND (MICROB? OR L25 OR CULTUR?) | |
| L39 | 11 | SEA FILE=WPIX ABB=ON | PLU=ON | L38 NOT L31 | |
| L40 | 1 | SEA FILE=WPIX ABB=ON | PLU=ON | L39 AND STIRRING/TI | 1 cite |

=> s 133 or 140

L80 5 L33 OR L40 5 cites total for WPIX

=> dup rem 149 167 158 179 180 removing duplicate citations
FILE 'MEDLINE' ENTERED AT 12:08:32 ON 28 JUL 2003

FILE 'CABA' ENTERED AT 12:08:32 ON 28 JUL 2003
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PROCESSING COMPLETED FOR L49
PROCESSING COMPLETED FOR L67
PROCESSING COMPLETED FOR L58
PROCESSING COMPLETED FOR L79

PROCESSING COMPLETED FOR L80

L81 17 DUP REM L49 L67 L58 L79 L80 (2 DUPLICATES REMOVED) *17 cites total*
 ANSWERS '1-2' FROM FILE MEDLINE
 ANSWER '3' FROM FILE CABA
 ANSWERS '4-6' FROM FILE BIOTECHNO
 ANSWERS '7-12' FROM FILE HCAPLUS
 ANSWERS '13-17' FROM FILE WPIX

=> d ibib abs ind 1-2 *indexing*

L81 ANSWER 1 OF 17 MEDLINE on STN
 ACCESSION NUMBER: 74298770 MEDLINE
 DOCUMENT NUMBER: 74298770 PubMed ID: 4850775
 TITLE: **Biogenesis** of beta-carotene in *Mycobacterium*
kansasii.
 AUTHOR: David H L
 SOURCE: JOURNAL OF BACTERIOLOGY, (1974 Aug) 119 (2) 527-33.
 Journal code: 2985120R. ISSN: 0021-9193.
 Report No.: NASA-74298770.
 PUB. COUNTRY: United States
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals; Space Life Sciences
 ENTRY MONTH: 197410
 ENTRY DATE: Entered STN: 19900310
 Last Updated on STN: 19900310
 Entered Medline: 19741025

CT Acetates: ME, metabolism
 Amines: PD, pharmacology
 Biogenesis
 Carbon Radioisotopes
 *Carotenoids: BI, biosynthesis
 Chloramphenicol: PD, pharmacology
 Chromatography, Thin Layer
 Darkness
 Light
 *Mycobacterium: ME, metabolism
 Oxygen
 RNA, Bacterial: BI, biosynthesis
 Rifampin: PD, pharmacology
 Spectrophotometry
 Temperature
 Time Factors
 Tritium
 Uracil: ME, metabolism

*no abstract given
 for 1st 2 citations*

RN 10028-17-8 (Tritium); 13292-46-1 (Rifampin); 36-88-4 (Carotenoids);
 56-75-7 (Chloramphenicol); 66-22-8 (Uracil); 7782-44-7 (Oxygen)
 CN 0 (Acetates); 0 (Amines); 0 (Carbon Radioisotopes); 0 (RNA, Bacterial)

L81 ANSWER 2 OF 17 MEDLINE on STN
 ACCESSION NUMBER: 73227417 MEDLINE
 DOCUMENT NUMBER: 73227417 PubMed ID: 4665108
 TITLE: Studies on natural photo-protectors. II. The influence of
 oxygen and temperature on photosensitivity of mutants of
Aspergillus giganteus with various ability of
 carotenoid synthesis.
 AUTHOR: Lazarski R
 SOURCE: FOLIA BIOLOGICA, (1972) 20 (3) 279-86.
 Journal code: 2984758R. ISSN: 0015-5497.
 PUB. COUNTRY: Poland

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 197310
 ENTRY DATE: Entered STN: 19900310
 Last Updated on STN: 19900310
 Entered Medline: 19731005

CT Aerobiosis
 Anaerobiosis
 *Aspergillus: ME, metabolism
 *Carotenoids: BI, biosynthesis
 Genetics, Microbial
 *Light
 Mutation
 *Oxygen
 *Temperature
 RN 36-88-4 (Carotenoids); 7782-44-7 (Oxygen)

=> d ibib abs ind 3

L81 ANSWER 3 OF 17 CABA COPYRIGHT 2003 CABI on STN

ACCESSION NUMBER: 83:112346 CABA
 DOCUMENT NUMBER: 831980736
 TITLE: The role of oxygen concentration in the synthesis of
carotenoids, poly- beta -hydroxybutyrate and
succinate oxidase in continuous
culture of Azospirillum
 AUTHOR: Nur, I.; Okon, Y.; Henis, Y.
 CORPORATE SOURCE: Dep. of Plant Path. and Microbiology, Hebrew Univ.
 of Jerusalem, P.O. Box 12, Rehovot 76100, Israel.
 SOURCE: Israel Journal of Botany, (1982) Vol. 31, No. 1-4,
 pp. 221-227. 19 ref.
 ISSN: 0021-213X
 DOCUMENT TYPE: Conference Article; Journal
 LANGUAGE: English

AB Azospirillum brasilense strain Cd was grown in ammonium-malate-mineral
 salts medium under various dissolved oxygen tensions. Maximum poly- beta
 -hydroxybutyrate content was observed under microaerobic conditions and
 intermediate dilution rates. Highest cell yield and respiration rate were
 obtained at relatively low oxygen. Protein content was higher at high
oxygen levels. Succinate oxidase and succinate
 dehydrogenase activities were especially high under high oxygen. Four
carotenoids were isolated and purified from membranes. In the
 presence of diphenylamine which inhibits **carotenoid** synthesis,
 the rate of acetylene reduction decreased to 50% of the control. In liquid
cultures, **carotenoid** synthesis was initiated only after
 the depletion of NH₄Cl when N₂ fixing activity became evident.
Carotenoids appeared to protect nitrogenase from oxidative damage.
 CC EE110 Agricultural Economics; DD500 Laws and Regulations; DD100
 Administration of Agencies and Organizations; CC200 Extension and Advisory
 Work; UU000 Sociology (General); JJ100 Soil Biology
 BT prokaryotes; Azospirillum; Spirillaceae; Gracilicutes; bacteria
 CT Nitrogen Fixation; enzymes; oxygen
 ST specific taxa
 RN 7782-44-7
 ORGN bacteria; Azospirillum brasilense

=> d ibib abs ind 4-6

L81 ANSWER 4 OF 17 BIOTECHNO COPYRIGHT 2003 Elsevier Science B.V. on STN
DUPLICATE

ACCESSION NUMBER: 1999:30021700 BIOTECHNO
TITLE: **Control** of both **foam** and dissolved **oxygen** in the presence of a surfactant for production of **.beta.-carotene** in *Blakeslea trispora*
AUTHOR: Seon-Won K.; Lee I.-Y.; Jeong J.-C.; Lee J.-H.; Park Y.-H.
CORPORATE SOURCE: I.-Y. Lee, Bioprocess Technol. Res. Division, Korea Res. Inst. of Biosci./Biotech., P.O. Box 115, Yusong, Taejeon 305-600, South Korea.
E-mail: leeiy@mail.kribb.re.kr
SOURCE: Journal of Microbiology and Biotechnology, (1999), 9/5 (548-553), 20 reference(s)
CODEN: JOMBES ISSN: 1017-7825
DOCUMENT TYPE: Journal; Article
COUNTRY: Korea, Republic of
LANGUAGE: English
SUMMARY LANGUAGE: English

AN 1999:30021700 BIOTECHNO

AB A production of **.beta.-carotene** was attempted in a fed-batch **culture** of *Blakeslea trispora* by **controlling** both foam and dissolved **oxygen** in the presence of surfactant, Span 20. Results obtained from the shake flask **cultures** indicated that a high **concentration** of dissolved **oxygen** was needed for both cell growth and **.beta.-carotene** synthesis, and the optimal concentration of glucose was found to be in the range of 50-100 g/l. In order to maintain the dissolved **oxygen concentration** level at higher than 50% of air saturation, pure **oxygen** was automatically sparged into the medium with air. Foam was controlled by bypassing air from the submerged **aeration** to the headspace in response to the foam that was caused by Span 20. High agitation speed was found to be detrimental to the cell growth due to shear damage, even though it provided sufficient dissolved **oxygen**. On the other hand, a low **aeration** speed caused stagnant regions in the **fermentor** because of improper mixing. Thus, for the fed-batch operation, agitation speed was increased gradually from 300 to 700 rpm to prevent cell damage at the initial stage of **fermentation** and to give efficient mixing for a viscous **culture** broth as the **culture** proceeded. By **controlling** dissolved **oxygen** and foam, a high **concentration** of **.beta.-carotene** (1,190 mg/l) was obtained in 6 days of the fed-batch **culture** of *B. trispora* with 2.5% of the dry cell weight, which was approximately 5 times higher than that of the batch **cultures**.

CT *dissolved **oxygen**; *surfactant; *sorbitan laurate; *beta **carotene**; *biotechnology; *protein synthesis; * **fermentation**; *fungus; *blakeslea trispora; glucose; foam; **oxygen concentration**; shear stress; bioreactor; fungus mutant; light exposure; oxidative stress; centrifugation; high performance liquid chromatography; mycelium; cell growth; nonhuman; article

RN (sorbitan laurate) 1338-39-2; (beta **carotene**) 7235-40-7; (glucose) 50-99-7, 84778-64-3

L81 ANSWER 5 OF 17 BIOTECHNO COPYRIGHT 2003 Elsevier Science B.V. on STN
DUPLICATE

ACCESSION NUMBER: 1997:27485777 BIOTECHNO

TITLE: Influence of **oxygen** and glucose on primary metabolism and astaxanthin production by *Phaffia rhodozyma* in batch and fed-batch **cultures**: Kinetic and **stoichiometric** analysis

AUTHOR: Yamane Y.-I.; Higashida K.; Nakashimada Y.; Kakizono T.; Nishio N.

CORPORATE SOURCE: N. Nishio, Fermentation Technology Department, Faculty of Engineering, Hiroshima University, Kagamiyama 1-4-1, Higashi-Hiroshima 739, Japan.
E-mail: nnishio@ipc.hiroshima-u.ac.jp

SOURCE: Applied and Environmental Microbiology, (1997), 63/11 (4471-4478), 35 reference(s)
CODEN: AEMIDF ISSN: 0099-2240

DOCUMENT TYPE: Journal; Article

COUNTRY: United States

LANGUAGE: English

SUMMARY LANGUAGE: English

AN 1997:27485777 BIOTECHNO

AB The influence of the **oxygen** and glucose supply on primary metabolism (**fermentation**, respiration, and anabolism) and astaxanthin production in the yeast *Phaffia rhodozyma* was investigated. When *P. rhodozyma* grew under **fermentative** conditions with limited **oxygen** or high **concentrations** of glucose, the astaxanthin production rate decreased remarkably. On the other hand, when the yeast grew under **aerobic** conditions, the astaxanthin production rate increased with increasing **oxygen** uptake. A kinetic analysis showed that the respiration rate correlated positively with the astaxanthin production rate, whereas there was a negative correlation with the ethanol production rate. The influence of glucose concentration at a fixed nitrogen **concentration** with a high level of **oxygen** was then investigated. The results showed that astaxanthin production was enhanced by an initial high carbon/nitrogen ratio (C/N ratio) present in the medium, but cell growth was inhibited by a high glucose concentration. A stoichiometric analysis suggested that astaxanthin production was enhanced by decreasing the amount of NADPH required for anabolism, which could be achieved by the repression of protein biosynthesis with a high C/N ratio. Based on these results, we performed a two-stage fed-batch **culture**, in which cell growth was enhanced by a low C/N ratio in the first stage and astaxanthin production was enhanced by a high C/N ratio in the second stage. In this **culture** system, the highest astaxanthin production, 16.0 mg per liter, was obtained.

CT *astaxanthin; *phaffia rhodozyma; *yeast; carbon; **carotenoid**; glucose; nitrogen; **oxygen**; reduced nicotinamide adenine dinucleotide phosphate; article; **culture** medium; fungus **culture**; fungus growth; kinetics; nonhuman; stoichiometry

RN (astaxanthin) 472-61-7; (carbon) 7440-44-0; (glucose) 50-99-7, 84778-64-3; (nitrogen) 7727-37-9; (**oxygen**) 7782-44-7; (reduced nicotinamide adenine dinucleotide phosphate) 53-57-6

L81 ANSWER 6 OF 17 BIOTECHNO COPYRIGHT 2003 Elsevier Science B.V. on STN

ACCESSION NUMBER: 1999:29160364 BIOTECHNO

TITLE: Effect of **culture** condition on the biosynthesis of **carotenoids** in *Rhodotorula glutinis* No. 21

AUTHOR: Sakaki H.; Nochide H.; Nakanishi T.; Miki W.; Fujita T.; Komemushi S.

CORPORATE SOURCE: H. Sakaki, Department of Agricultural Chemistry, Faculty of Agriculture, Kinki University, 3327-204 Nakamachi, Nara 631-8505, Japan.

SOURCE: Seibutsu-kogaku Kaishi, (1999), 77/2 (55-59), 13
reference(s)
CODEN: SEKAEA ISSN: 0919-3758

DOCUMENT TYPE: Journal; Article
COUNTRY: Japan
LANGUAGE: Japanese
SUMMARY LANGUAGE: English; Japanese

AN 1999:29160364 BIOTECHNO

AB Changes in the biosynthesis of **carotenoids** caused by altering the **culture** conditions of the yeast *Rhodotorula glutinis* No. 21 were investigated. Cells grown on lactate showed a higher production of torularhodin, one of the final products, compared with those grown on glucose, but no changes were observed as a result of adjusting the pH, at the start of the cultivation. These findings suggested that the difference in the carbon source was a factor giving rise to a change in the **carotenoid** biosynthesis system of *R. glutinis* No. 21. Increases in the contents of torulene and torularhodin were related to elevation of the dissolved **oxygen concentration**, which was adjusted by **aeration**. It was concluded that this yeast switches its system of **carotenoid** biosynthesis according to the extracellular conditions. The results obtained will contribute to elucidating the role of torularhodin in this non-phototrophic yeast which produces two **carotenoids**, **.beta.-carotene** and torularhodin, as the final products.

CT *biosynthesis; ***carotenoid**; *Rhodotorula glutinis*; lactic acid; torularhodin; glucose; pH; torulene; dissolved **oxygen**; **aeration**; **beta carotene**

=> d ibib abs hitrn ind 7-12

L81 ANSWER 7 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2003:320046 HCAPLUS
DOCUMENT NUMBER: 138:302755
TITLE: Microorganism and production of carotenoid compounds thereby

INVENTOR(S): Yamaoka, Yukiho
PATENT ASSIGNEE(S): National Institute of Advanced Industrial Science and Technology, Japan

SOURCE: PCT Int. Appl., 24 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|--|------|----------|-----------------|------------|
| WO 2003033683 | A1 | 20030424 | WO 2002-JP10619 | 20021011 |
| W: CN, US | | | | |
| RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR | | | | |
| JP 2003189846 | A2 | 20030708 | JP 2002-231126 | 20020808 |
| PRIORITY APPLN. INFO.: | | | | |
| | | | JP 2001-318746 | A 20011016 |
| | | | JP 2002-132190 | A 20020507 |
| | | | JP 2002-231126 | A 20020808 |

AB Astaxanthin and canthaxanthin are manufd. com. with marine *Thraustochytrium* sp. CHN-3 (FERM P-18556) of *Labyrinthula* by aerobic fermn. under illumination. The astaxanthin and canthaxanthin are isolated from the microorganism by solvent extn. and chromatog.

- IT 7782-44-7, Oxygen, biological studies
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
 (Uses)
 (astaxanthin and canthaxanthin manuf. with marine Thraustochytrium)
- IC ICM C12N001-14
 ICS C12P023-00; C12R001-645
- CC 16-2 (Fermentation and Bioindustrial Chemistry)
 Section cross-reference(s): 1, 17, 63
- ST astaxanthin canthaxanthin manuf Thraustochytrium Labyrinthula culture
 medium
- IT **Fermentation**
 (aerobic; astaxanthin and canthaxanthin manuf. with marine
 Thraustochytrium)
- IT Carbon sources, microbial
Culture media
 Feed
 Health food
 Illumination
 Labyrinthula
 Nitrogen sources, microbial
 Seawater
 Solvent extraction
 Thraustochytrium
 pH
 (astaxanthin and canthaxanthin manuf. with marine Thraustochytrium)
- IT **Carotenes, preparation**
 RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP
 (Preparation)
 (astaxanthin and canthaxanthin manuf. with marine Thraustochytrium)
- IT Vitamins
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
 (Uses)
 (astaxanthin and canthaxanthin manuf. with marine Thraustochytrium)
- IT Light
 (blue; astaxanthin and canthaxanthin manuf. with marine
 Thraustochytrium)
- IT Light
 (red; astaxanthin and canthaxanthin manuf. with marine Thraustochytrium)
- IT 50-99-7, D-Glucose, biological studies 57-13-6, Urea, biological studies
 57-48-7, D-Fructose, biological studies 57-50-1, Sucrose, biological
 studies 59-43-8, Thiamine, biological studies 67-56-1, Methyl alcohol,
 biological studies 67-64-1, Acetone, biological studies 67-66-3,
 Chloroform, biological studies 7664-41-7, Ammonia, biological studies
 7757-79-1, Potassium nitrate, biological studies 7782-44-7,
 Oxygen, biological studies
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
 (Uses)
 (astaxanthin and canthaxanthin manuf. with marine Thraustochytrium)

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS
 RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L81 ANSWER 8 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2002:181867 HCAPLUS

DOCUMENT NUMBER: 138:236950

TITLE: Effect of the aeration rate and agitation speed on
 .beta.-carotene production and morphology of *Blakeslea*
trisporea in a stirred tank reactor: mathematical
 modeling

AUTHOR(S): Mantzouridou, F.; Roukas, T.; Kotzekidou, P.
 CORPORATE SOURCE: Department of Food Science and Technology, Aristotle

University of Thessaloniki, Thessaloniki, 54006,
Greece
SOURCE: Biochemical Engineering Journal (2002), 10(2), 123-135
CODEN: BEJOFV; ISSN: 1369-703X
PUBLISHER: Elsevier Science S.A.
DOCUMENT TYPE: Journal
LANGUAGE: English

- AB The effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of *Blakeslea trispora* in a stirred tank reactor was investigated. *B. trispora* formed hyphae, zygothores and zygosporos during the fermn. The zygosporos were the morphol. form responsible for .beta.-carotene prodn. Both aeration and agitation significantly affected .beta.-carotene concn., productivity, biomass and the volumetric mass transfer coeff. (KLa). The highest .beta.-carotene concn. (1.5 kg m⁻³) and the highest productivity (0.08 kg m⁻³ per day) were obtained at low impeller speed (150 rpm) and high aeration rate (1.5 vvm). Also, max. productivity (0.08 kg m⁻³ per day) and biomass dry wt. (26.4 kg m⁻³) were achieved at high agitation speed (500 rpm) and moderate aeration rate (1.0 vvm). Conversely, the highest value of KLa (0.33 s⁻¹) was obsd. at high agitation speed (500 rpm) and high aeration rate (1.5 vvm). The expts. were arranged according to a central composite statistical design. Response surface methodol. was used to describe the effect of impeller speed and aeration rate on the most important fermn. parameters. In all cases, the fit of the model was found to be good. All fermn. parameters (except biomass concn.) were strongly affected by the interactions among the operation variables. .beta.-Carotene concn. and productivity were significantly influenced by the aeration, agitation, and by the pos. or neg. quadratic effect of the aeration rate. Biomass concn. was principally related to the aeration rate, agitation speed, and the pos. or neg. quadratic effect of the impeller speed and aeration rate, resp. Finally, the volumetric mass transfer coeff. was characterized by the significant effect of the agitation speed, while the aeration rate had a small effect on KLa.
- IT 7782-44-7, Oxygen, processes
RL: BCP (Biochemical process); BIOL (Biological study); PROC (Process)
(dissolved; modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of *Blakeslea trispora* in stirred tank reactor)
- IT 7235-40-7P, .beta.-Carotene
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of *Blakeslea trispora* in stirred tank reactor)
- CC 16-2 (Fermentation and Bioindustrial Chemistry)
- ST *Blakeslea beta carotene* fermn aeration agitation model
- IT Fermentation
(batch; modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of *Blakeslea trispora* in stirred tank reactor)
- IT Mass transfer
(gas-liq., KLa; modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of *Blakeslea trispora* in stirred tank reactor)
- IT Aeration
Agitation (mechanical)
Blakeslea trispora
Cell morphology
Simulation and Modeling, biological
(modeling of the effect of aeration rate and agitation speed on

.beta.-carotene prodn. and morphol. of Blakeslea trispora in stirred tank reactor)

IT Optimization
(statistical; modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of Blakeslea trispora in stirred tank reactor)

IT Fermentation apparatus
(stirred-tank fermentor; modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of Blakeslea trispora in stirred tank reactor)

IT 7782-44-7, Oxygen, processes
RL: BCP (Biochemical process); BIOL (Biological study); PROC (Process)
(dissolved; modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of Blakeslea trispora in stirred tank reactor)

IT 7235-40-7P, .beta.-Carotene
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(modeling of the effect of aeration rate and agitation speed on .beta.-carotene prodn. and morphol. of Blakeslea trispora in stirred tank reactor)

REFERENCE COUNT: 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L81 ANSWER 9 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:924027 HCAPLUS
DOCUMENT NUMBER: 136:52783
TITLE: Process for producing carotenoid pigments
INVENTOR(S): Tsubokura, Akira; Mizuta, Haruyoshi
PATENT ASSIGNEE(S): Nippon Mitsubishi Oil Corporation, Japan
SOURCE: PCT Int. Appl., 23 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|------|----------|-----------------|----------|
| WO 2001096591 | A1 | 20011220 | WO 2001-JP4874 | 20010608 |
| W: AU, CA, CN, IL, KR, US RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR | | | | |
| JP 2001352995 | A2 | 20011225 | JP 2000-175124 | 20000612 |
| AU 2001062730 | A5 | 20011224 | AU 2001-62730 | 20010608 |
| EP 1229126 | A1 | 20020807 | EP 2001-936932 | 20010608 |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY, TR | | | | |
| US 2003044886 | A1 | 20030306 | US 2002-49228 | 20020211 |
| PRIORITY APPLN. INFO.: JP 2000-175124 A 20000612 WO 2001-JP4874 W 20010608 | | | | |

AB A process for the microbial manuf. of carotenoids of desired ratio of carotenoid compds. with bacteria E-396 and A-581-1 which have low growth rate and enable easy isolation of the carotenoids was given. The ratio of the carotenoid compds. (i.e., astaxanthin, adonixanthin, .beta.-carotene, echinenone, canthaxanthin, zeaxanthin, .beta.-cryptoxanthin, 3-hydroxyechinenone, adonirubin, etc.) is controlled by the concn. of oxygen dissolved in a liq. culture medium during the fermn.

IT 144-68-3P, Zeaxanthin 432-68-8P, Echinenone
472-61-7P, Astaxanthin 472-70-8P, .beta.-Cryptoxanthin

514-78-3P, Canthaxanthin 4339-77-9P, 3-Hydroxyechinenone

4418-72-8P, Adonirubin 4418-73-9P, Adonixanthin

7235-40-7P, .beta.-Carotene

RL: BPN (Biosynthetic preparation); BIOL (Biological study); **PREP (Preparation)**

(process for producing carotenoid pigments)

IT 7782-44-7, Oxygen, biological studies

RL: BSU (Biological study, unclassified); BIOL (Biological study)

(process for producing carotenoid pigments)

IC ICM C12P023-00

CC 16-2 (Fermentation and Bioindustrial Chemistry)

ST carotenoid manuf bacteria dissolved oxygen

IT rRNA

RL: BSU (Biological study, unclassified); BIOL (Biological study)

(16 S, gene for; process for producing carotenoid pigments)

IT Bacteria (Eubacteria)

Culture media

DNA sequences

Fermentation

Taxonomy

(process for producing carotenoid pigments)

IT **Carotenes, preparation**

RL: BPN (Biosynthetic preparation); BIOL (Biological study); **PREP**

(Preparation)

(process for producing carotenoid pigments)

IT Gene, microbial

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL

(Biological study)

(process for producing carotenoid pigments)

IT 382660-64-2 382660-65-3

RL: PRP (Properties)

(nucleotide sequence; process for producing carotenoid pigments)

IT 144-68-3P, Zeaxanthin 432-68-8P, Echinenone

472-61-7P, Astaxanthin 472-70-8P, .beta.-Cryptoxanthin

514-78-3P, Canthaxanthin 4339-77-9P, 3-Hydroxyechinenone

4418-72-8P, Adonirubin 4418-73-9P, Adonixanthin

7235-40-7P, .beta.-Carotene

RL: BPN (Biosynthetic preparation); BIOL (Biological study); **PREP (Preparation)**

(process for producing carotenoid pigments)

IT 7782-44-7, Oxygen, biological studies

RL: BSU (Biological study, unclassified); BIOL (Biological study)

(process for producing carotenoid pigments)

REFERENCE COUNT: 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L81 ANSWER 10 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:691371 HCAPLUS

DOCUMENT NUMBER: 135:370671

TITLE: Application of a complete factorial design for the production of zeaxanthin by *Flavobacterium* sp.

AUTHOR(S): Masetto, Alejandra; Flores-Cotera, Luis B.; Diaz, Carlos; Langley, Elizabeth; Sanchez, Sergio

CORPORATE SOURCE: Departamento de Biologia Molecular y Biotecnologia del Instituto de Investigaciones Biomedicas, Universidad Nacional Autonoma de Mexico, Mexico, 04510, Mex.

SOURCE: Journal of Bioscience and Bioengineering (2001), 92(1), 55-58

CODEN: JBBIF6; ISSN: 1389-1723

PUBLISHER: Society for Bioscience and Bioengineering, Japan

DOCUMENT TYPE: Journal
 LANGUAGE: English

AB Utilizing a four-liter fermentor and applying a complete factorial design 23, the combined effects of agitation speed, aeration rate, and corn steep liquor concn. on zeaxanthin prodn. by *Flavobacterium* sp. were studied. Maximum growth and prodn. of total carotenoids and zeaxanthin were obtained at 600 rpm, 2 vvm and 4.6% corn steep liquor. Under these conditions, zeaxanthin represented 86% of the total carotenoids produced. Lower values of the variables studied resulted in lower growth, volumetric prodn. of zeaxanthin and total carotenoids, and favored the formation of other carotenoids such as .beta.-carotene and canthaxanthin. The pos. effects on growth and total carotenoids and zeaxanthin formation were in a large extent due to the interaction of agitation/corn steep liquor. However, aeration also had a pos. effect on growth.

IT 144-68-3P, Zeaxanthin 514-78-3P, Canthaxanthin

7235-40-7P, .beta.-Carotene

RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP

(Preparation)

(application of complete factorial design for prodn. of zeaxanthin by *Flavobacterium* sp.)

IT 7782-44-7, Oxygen, biological studies

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(dissolved; application of complete factorial design for prodn. of zeaxanthin by *Flavobacterium* sp.)

CC 16-2 (Fermentation and Bioindustrial Chemistry)

ST *Flavobacterium* zeaxanthin fermn optimization

IT Fermentation

(aerobic; application of complete factorial design for prodn. of zeaxanthin by *Flavobacterium* sp.)

IT Aeration

Agitation (mechanical)

Flavobacterium

Growth, microbial

(application of complete factorial design for prodn. of zeaxanthin by *Flavobacterium* sp.)

IT Carotenes, preparation

RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP

(Preparation)

(application of complete factorial design for prodn. of zeaxanthin by *Flavobacterium* sp.)

IT Industrial liquors

(corn steep liquor; application of complete factorial design for prodn. of zeaxanthin by *Flavobacterium* sp.)

IT Optimization

(statistical; application of complete factorial design for prodn. of zeaxanthin by *Flavobacterium* sp.)

IT 144-68-3P, Zeaxanthin 514-78-3P, Canthaxanthin

7235-40-7P, .beta.-Carotene

RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP

(Preparation)

(application of complete factorial design for prodn. of zeaxanthin by *Flavobacterium* sp.)

IT 7782-44-7, Oxygen, biological studies

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(dissolved; application of complete factorial design for prodn. of zeaxanthin by *Flavobacterium* sp.)

REFERENCE COUNT:

15

THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L81 ANSWER 11 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN
 ACCESSION NUMBER: 2002:118119 HCAPLUS
 DOCUMENT NUMBER: 136:133689
 TITLE: Production of .beta.-carotene from Blakeslea trispora
 INVENTOR(S): Park, Yeong Hoon; Lee, In Yeong; Kim, Seon Won; Lee, Jung Heon; Jeong, Jae Cheol
 PATENT ASSIGNEE(S): Korea Institute of Science and Technology, S. Korea
 SOURCE: Repub. Korean Kongkae Taeho Kongbo, No pp. given
 CODEN: KRXXA7
 DOCUMENT TYPE: Patent
 LANGUAGE: Korean
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------------------------|------|----------|-----------------|----------|
| KR 2000031738 | A | 20000605 | KR 1998-47930 | 19981110 |
| PRIORITY APPLN. INFO.: | | | KR 1998-47930 | 19981110 |

AB Addn. of a surfactant in the medium to increase the prodn. of .beta.-carotene by a Blakeslea trispora culture causes foaming during fermn. An anti-foaming agent can be used to control foam, but it inhibits the growth of the fungi. Submerged aeration accompanied with surface aeration and control of stirring speed can be used effectively to control foam and increase the yield of .beta.-carotene from Blakeslea. In the fermn. process, the anti-foam agent, Span 20 is used to control foam. In addn. to anti-foam agent, submerged and surface aeration are applied to control foam. The total aeration rate is controlled in the range of 0.5-3.0 L air/L medium/min depending on the growth state of fungi. The speed of stirring is increased stepwise in the range of 10-100 rpm reached at 150-800 rpm depending on the increase of cell mass. The main source of carbon is glucose and the optimal concn. is kept under 70 g/L supplied intermittently. Pure oxygen is supplied to increase the dissolved oxygen in the medium. The final yield of .beta.-carotene is 17 g/L.

IT **7235-40-7P, .beta.-Carotene**
 RL: BMF (Bioindustrial manufacture); BIOL (Biological study); **PREP (Preparation)**
 (prodn. of .beta.-carotene from Blakeslea trispora)

IC ICM C12P023-00
 CC 16-2 (Fermentation and Bioindustrial Chemistry)
 ST Blakeslea beta carotene fermn foam control
 IT **Fermentation**
 (fed-batch; prodn. of .beta.-carotene from Blakeslea trispora)

IT **Aeration**
 Agitation (mechanical)
 Blakeslea trispora
 Foaming
 (prodn. of .beta.-carotene from Blakeslea trispora)

IT **7235-40-7P, .beta.-Carotene**
 RL: BMF (Bioindustrial manufacture); BIOL (Biological study); **PREP (Preparation)**
 (prodn. of .beta.-carotene from Blakeslea trispora)

IT 1338-39-2, Span 20
 RL: BUU (Biological use, unclassified); BIOL (Biological study); **USES (Uses)**
 (prodn. of .beta.-carotene from Blakeslea trispora)

L81 ANSWER 12 OF 17 HCAPLUS COPYRIGHT 2003 ACS on STN
 ACCESSION NUMBER: 1994:215496 HCAPLUS
 DOCUMENT NUMBER: 120:215496

TITLE: Fermentative manufacture of .beta.-carotene.
 INVENTOR(S): Matsumura, Shigeo; Sumino, Yasuhiro; Matsui, Junji
 PATENT ASSIGNEE(S): Takeda Chemical Industries, Ltd., Japan
 SOURCE: Eur. Pat. Appl., 12 pp.
 CODEN: EPXXDW
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|------|----------|-----------------|----------|
| EP 586255 | A1 | 19940309 | EP 1993-306964 | 19930902 |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, NL, PT, SE | | | | |
| CA 2105527 | AA | 19940304 | CA 1993-2105527 | 19930903 |
| JP 06153986 | A2 | 19940603 | JP 1993-219427 | 19930903 |
| PRIORITY APPLN. INFO.: | | | JP 1992-236176 | 19920903 |

AB .beta.-Carotene is manufd. using a microalga tolerant to an active O generator, such as methylene blue and rose bengal, and capable of producing .beta.-carotene. The microalga is preferably Chlorella pyrenoidosa.
 IT 7235-40-7P, .beta.-Carotene
 RL: BMF (Bioindustrial manufacture); BIOL (Biological study); **PREP (Preparation)**
 (manuf. of, fermentative, with Chlorella pyrenoidosa)
 IT 7782-44-7, Oxygen, biological studies
 RL: BIOL (Biological study)
 (singlet, in fermentative .beta.-carotene manuf., with Chlorella pyrenoidosa)
 IC ICM C12P023-00
 ICS C12N001-12
 ICI C12P023-00, C12R001-89
 CC 16-8 (Fermentation and Bioindustrial Chemistry)
 ST fermn Chlorella beta carotene
 IT Chlorella pyrenoidosa
 (.beta.-carotene manuf. by fermn. with)
 IT **Fermentation**
 (.beta.-carotene, with Chlorella pyrenoidosa)
 IT 61-73-4, Methylene blue 11121-48-5, Rose bengal
 RL: BIOL (Biological study)
 (in fermentative .beta.-carotene manuf., with Chlorella pyrenoidosa)
 IT 7235-40-7P, .beta.-Carotene
 RL: BMF (Bioindustrial manufacture); BIOL (Biological study); **PREP (Preparation)**
 (manuf. of, fermentative, with Chlorella pyrenoidosa)
 IT 7782-44-7, Oxygen, biological studies
 RL: BIOL (Biological study)
 (singlet, in fermentative .beta.-carotene manuf., with Chlorella pyrenoidosa)

=> d ibib abs 13-17

L81 ANSWER 13 OF 17 WPIX COPYRIGHT 2003 THOMSON DERWENT on STN
 ACCESSION NUMBER: 1998-467550 [40] WPIX
 DOC. NO. CPI: C1998-141821
 TITLE: **Fermentative production of valuable compound(s)**
 - by **fermentation** of a **microbial**
 strain on an industrial scale using a **chemically**
defined medium and recovery of the compound(s).

DERWENT CLASS: B04 D16
 INVENTOR(S): DE LAAT, W T A; KOEKMAN, B P; PREUSTING, J C G; DE LAAT, W T A M
 PATENT ASSIGNEE(S): (KONN) GIST-BRÖCADES BV; (STAM) DSM NV; (DLAA-I) DE LAAT W T A M; (KOEK-I) KOEKMAN B P; (PREU-I) PREUSTING J C G
 COUNTRY COUNT: 82
 PATENT INFORMATION:

| PATENT NO | KIND | DATE | WEEK | LA | PG |
|--|------|----------|-----------|----|----|
| WO 9837179 | A2 | 19980827 | (199840)* | EN | 37 |
| RW: AT BE CH DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW | | | | | |
| W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM GW HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW | | | | | |
| AU 9864000 | A | 19980909 | (199905) | | |
| EP 970236 | A2 | 20000112 | (200008) | EN | |
| R: AL AT BE CH DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI | | | | | |
| CZ 9902954 | A3 | 20000412 | (200026) | | |
| BR 9807362 | A | 20000418 | (200032) | | |
| CN 1248294 | A | 20000322 | (200032) | | |
| KR 2000075487 | A | 20001215 | (200131) | | |
| MX 9907691 | A1 | 20000601 | (200133) | | |
| JP 2001512970 | W | 20010828 | (200156) | | 44 |
| US 2002039758 | A1 | 20020404 | (200227) | | |

APPLICATION DETAILS:

| PATENT NO | KIND | APPLICATION | DATE |
|---------------|-----------|----------------|----------|
| WO 9837179 | A2 | WO 1998-EP1122 | 19980220 |
| AU 9864000 | A | AU 1998-64000 | 19980220 |
| EP 970236 | A2 | EP 1998-909483 | 19980220 |
| | | WO 1998-EP1122 | 19980220 |
| CZ 9902954 | A3 | WO 1998-EP1122 | 19980220 |
| | | CZ 1999-2954 | 19980220 |
| BR 9807362 | A | BR 1998-7362 | 19980220 |
| | | WO 1998-EP1122 | 19980220 |
| CN 1248294 | A | CN 1998-802632 | 19980220 |
| KR 2000075487 | A | WO 1998-EP1122 | 19980220 |
| | | KR 1999-707546 | 19990819 |
| MX 9907691 | A1 | MX 1999-7691 | 19990819 |
| JP 2001512970 | W | JP 1998-536284 | 19980220 |
| | | WO 1998-EP1122 | 19980220 |
| US 2002039758 | A1 Div ex | US 1999-367029 | 19991025 |
| | | US 2001-982474 | 20011017 |

FILING DETAILS:

| PATENT NO | KIND | PATENT NO |
|---------------|-------------|------------|
| AU 9864000 | A Based on | WO 9837179 |
| EP 970236 | A2 Based on | WO 9837179 |
| CZ 9902954 | A3 Based on | WO 9837179 |
| BR 9807362 | A Based on | WO 9837179 |
| KR 2000075487 | A Based on | WO 9837179 |
| JP 2001512970 | W Based on | WO 9837179 |

PRIORITY APPLN. INFO: EP 1997-200494 19970220

AN 1998-467550 [40] WPIX

AB WO 9837179 A UPAB: 19981008

A process for the production of a valuable compound comprises: (a) **fermentation** of a **microbial** strain of an industrial scale in a **fermentation** medium which is a chemically defined medium composed of chemically defined constituents; and (b) recovery of the valuable compound from the **fermentation** broth.

Also claimed is a method for preparing and/or improving a **microbial** strain producing a valuable compound of interest which is capable of being **fermented** on an industrial scale in a chemically defined medium, comprising: (a) subjecting a suitable parent strain to a mutagenic treatment selected from physical mutagens and chemical mutagens, and/or to DNA transformation; (b) screening the resulting mutants and/or transformants for their growth performance on a chemically defined medium and their production level of the valuable compound of interest; (c) selecting mutants and/or transformants which have a good growth performance on a chemically defined medium and/or an improved production level of the valuable compound of interest as compared to the parent strain.

USE - The method can be used for the production of valuable compounds such as beta-lactam compounds, enzymes, astaxanthin, arachidonic acid, triglycerides, beta-**carotene**, glucose isomerase (GI), clavulanic acid or erythromycin (claimed).

ADVANTAGE - The productivity of **microbial** strains in chemically defined media, when measured on an industrial scale, may be comparable to or in some cases even higher than their productivity in complex media. **Oxygen** transfer from the gas phase to the liquid phase and the carbon dioxide transfer from the liquid phase to the gas phase is improved substantially as compared to using complex media. The use of chemically defined media has a favourable influence on morphology, i.e. by producing a more rigid pellet which does not easily fall apart during **fermentation**. In addition, the chemically defined medium can decrease the viscosity of filamentous **fermentation** broths and improve downstream processing.

Dwg.0/2

L81 ANSWER 14 OF 17 WPIX COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: 1995-053688 [08] WPIX

DOC. NO. CPI: C1995-024479

TITLE: New bacteria which produce **carotenoid** pigments
- used for the prodn. of astaxanthin, adonixanthin, beta-**carotene**, echinenone, **canthaxanthin** and zeaxanthin.

DERWENT CLASS: B04 B05 D13 D16 D21 E24

INVENTOR(S): KIYOTA, T; TAKAKI, M; TSUBOKURA, A; YONEDA, H

PATENT ASSIGNEE(S): (NIOC) NIPPON OIL KK; (MISQ) NIPPON MITSUBISHI OIL CORP;
(NIOC) NIPPON OIL CO LTD; (NIOC) NIPPON MITSUBISHI OIL CORP

COUNTRY COUNT: 9

PATENT INFORMATION:

| PATENT NO | KIND | DATE | WEEK | LA | PG |
|-------------------|------|----------|-----------|----|----|
| EP 635576 | A1 | 19950125 | (199508)* | EN | 29 |
| R: CH DE FR GB LI | | | | | |
| NO 9402731 | A | 19950123 | (199511) | | |
| CA 2128549 | A | 19950123 | (199516) | | |
| JP 07079796 | A | 19950328 | (199521) | | 20 |

US 5607839 A 19970304 (199715) 16
 US 5858761 A 19990112 (199910)
 EP 635576 B1 20000830 (200042) EN
 R: CH DE FR GB LI
 DE 69425706 E 20001005 (200057)
 JP 3242531 B2 20011225 (200203) 20
 NO 313204 B1 20020826 (200263)

APPLICATION DETAILS:

| PATENT NO | KIND | APPLICATION | DATE |
|-------------|----------|-----------------|----------|
| EP 635576 | A1 | EP 1994-111525 | 19940722 |
| NO 9402731 | A | NO 1994-2731 | 19940721 |
| CA 2128549 | A | CA 1994-2128549 | 19940721 |
| JP 07079796 | A | JP 1994-152240 | 19940704 |
| US 5607839 | A | US 1994-276943 | 19940719 |
| US 5858761 | A Div ex | US 1994-276943 | 19940719 |
| | | US 1996-716841 | 19960919 |
| EP 635576 | B1 | EP 1994-111525 | 19940722 |
| DE 69425706 | E | DE 1994-625706 | 19940722 |
| | | EP 1994-111525 | 19940722 |
| JP 3242531 | B2 | JP 1994-152240 | 19940704 |
| NO 313204 | B1 | NO 1994-2731 | 19940721 |

FILING DETAILS:

| PATENT NO | KIND | PATENT NO |
|-------------|-------------------|-------------|
| US 5858761 | A Div ex | US 5607839 |
| DE 69425706 | E Based on | EP 635576 |
| JP 3242531 | B2 Previous Publ. | JP 07079796 |
| NO 313204 | B1 Previous Publ. | NO 9402731 |

PRIORITY APPLN. INFO: JP 1993-181615 19930722

AN 1995-053688 [08] WPIX

AB EP 635576 A UPAB: 19950301

Bacteria belonging to a new genus and having the following properties are claimed: (1) morphology: polymorphic rod; (2) motility: motile; (3) flagella: peritrichous; (4) spore formation: none; (5) gram strain: negative; (6) prodn. of pigment: positive (water insoluble); (7) oxidase: positive; (8) catalase: positive; (9) behaviour toward oxygen: aerobic; (10) fermentation of glucose: negative; (11) prodn. of 3-ketolactose: negative; (12) quinone type: Q-10; (13) GC content of intracellular DNA: 64-69 molar %; (14) formation of slime: glucose, negative; sucrose, negative; (15) presence of sphingolipid: negative; (16) presence of bacteriochlorophyll: negative.

USE - The bacteria can be cultured to produce one or a mixt. of **carotenoid** pigments selected from astaxanthin, adonixanthin, beta-carotene, echinenone, canthaxanthin and zeaxanthin. The **carotenoid** pigments can be used as additives in food, feed, pharmaceuticals, cosmetics, etc.

ADVANTAGE - Using the bacteria, **carotenoids** can be produced on an industrial scale. They can produce natural type astaxanthin., Almost 100% of astaxanthin produced by the bacteria is (3S,3'S)-astaxanthin.
 Dwg.0/6

ABEQ US 5607839 A UPAB: 19970410

A new process for production of a **carotenoid** pigment selected from the group consisting of astaxanthin, adonixanthin, beta-carotene, echinenone, canthaxanthin, zeaxanthin and mixtures

thereof, comprising the steps of:

culturing bacterium strain E-396, FERM BP-4283, or A-581-1, FERM BP-4671, in an aqueous nutrient medium comprising sources of carbon, nitrogen, and inorganic substances and

recovering an individual carotenoid pigment or a mixture of the carotenoid pigments.

Dwg.0/6

L81 ANSWER 15 OF 17 WPIX COPYRIGHT 2003 THOMSON DERWENT on STN
 ACCESSION NUMBER: 1991-369260 [50] WPIX
 DOC. NO. CPI: C1991-159215
 TITLE: Continuous fermentation of carotenoid
 - producing microorganisms - by addn. of nutrient
 at rate needed for max. growth.
 DERWENT CLASS: D13 D16 E24
 INVENTOR(S): BAILEY, R B; MEDWID, R D
 PATENT ASSIGNEE(S): (COOA) COORS BIOTECH INC; (ZEAG-N) ZEAGEN INC; (UVFO-N)
 UNIVERSAL FOODS CORP; (ARCH) ARCHER-DANIELS MIDLAND CO
 COUNTRY COUNT: 32
 PATENT INFORMATION:

| PATENT NO | KIND | DATE | WEEK | LA | PG |
|--|------|----------|-----------|----|----|
| WO 9118108 | A | 19911128 | (199150)* | | 28 |
| RW: AT BE CH DE DK ES FR GB GR IT LU NL OA SE | | | | | |
| W: AT AU BB BG BR CA CH DE DK ES FI GB HU JP KP KR LK LU MC MW NL NO | | | | | |
| PL RO SD SE SU | | | | | |
| AU 9180820 | A | 19911210 | (199212) | | |
| BR 9106448 | A | 19930518 | (199324) | | |
| EP 553085 | A1 | 19930804 | (199331) | EN | 28 |
| R: DE ES FR GB GR IT NL | | | | | |
| JP 06500008 | W | 19940106 | (199406) | | 14 |
| EP 553085 | A4 | 19930901 | (199527) | | |
| EP 553085 | B1 | 19991020 | (199948) | EN | |
| R: DE ES FR GB GR IT NL | | | | | |
| DE 69131730 | E | 19991125 | (200002) | | |
| ES 2139577 | T3 | 20000216 | (200016) | | |
| JP 3065348 | B2 | 20000717 | (200039) | | 15 |

APPLICATION DETAILS:

| PATENT NO | KIND | APPLICATION | DATE |
|-------------|------|----------------|----------|
| BR 9106448 | A | BR 1991-6448 | 19910514 |
| | | WO 1991-US3358 | 19910514 |
| EP 553085 | A1 | EP 1991-910886 | 19910514 |
| | | WO 1991-US3358 | 19910514 |
| JP 06500008 | W | JP 1991-510821 | 19910514 |
| | | WO 1991-US3358 | 19910514 |
| EP 553085 | A4 | EP 1991-910886 | 19910514 |
| EP 553085 | B1 | EP 1991-910886 | 19910514 |
| | | WO 1991-US3358 | 19910514 |
| DE 69131730 | E | DE 1991-631730 | 19910514 |
| | | EP 1991-910886 | 19910514 |
| | | WO 1991-US3358 | 19910514 |
| ES 2139577 | T3 | EP 1991-910886 | 19910514 |
| JP 3065348 | B2 | JP 1991-510821 | 19910514 |
| | | WO 1991-US3358 | 19910514 |

FILING DETAILS:

| PATENT NO | KIND | | PATENT NO |
|-------------|------|----------------|-------------|
| BR 9106448 | A | Based on | WO 9118108 |
| EP 553085 | A1 | Based on | WO 9118108 |
| JP 06500008 | W | Based on | WO 9118108 |
| EP 553085 | B1 | Based on | WO 9118108 |
| DE 69131730 | E | Based on | EP 553085 |
| | | Based on | WO 9118108 |
| ES 2139577 | T3 | Based on | EP 553085 |
| JP 3065348 | B2 | Previous Publ. | JP 06500008 |
| | | Based on | WO 9118108 |

PRIORITY APPLN. INFO: US 1990-524140 19900515

AN 1991-369260 [50] WPIX

AB WO 9118108 A UPAB: 19960108

A continuous **fermentation** method for **carotenoid**

-producing heterotrophic microorganisms is claimed comprising (a) diluting a **fermentation** broth comprising the microorganism by continuously adding fresh **fermentation** medium comprising a nutrient to the **fermentation** broth so that the rate of addn. of the nutrient is less than that necessary to provide for a maximum growth rate of the microorganisms, (b) maintaining the pH of the **fermentation** broth at pH 5.5-6.5 and (c) maintaining the temp. at 30-38 deg.C.

The pref. microorganisms are algae of the species *Neosporangiococcum excentricum* (ATCC40355). The nutrient is pref. glucose or sucrose. The **fermentation** broth pref. contains greater than 10% dissolved oxygen and the partial pressure of CO₂ in the broth is pref. less than 0.04.

USE/ADVANTAGE - The process provides a high level of growth and productivity over an extended period of time. In particular, xanthophylls can be produced at levels of at least 20 mg/l/hr. The xanthophylls are useful as natural colouring agents, esp. as feed supplements for poultry. @ (28pp Dwg.No.0/0)

0/0

ABEQ EP 553085 A UPAB: 19931118

A continuous **fermentation** method for **carotenoid**

-producing heterotrophic microorganisms is claimed comprising (a) diluting a **fermentation** broth comprising the microorganism by continuously adding fresh **fermentation** medium comprising a nutrient to the **fermentation** broth so that the rate of addn. of the nutrient is less than that necessary to provide for a maximum growth rate of the microorganisms, (b) maintaining the pH of the **fermentation** broth at pH 5.5-6.5 and (c) maintaining the temp. at 30-38 deg.C.

The pref. microorganisms are algae of the species *Neosporangiococcum excentricum* (ATCC40355). The nutrient is pref. glucose or sucrose. The **fermentation** broth pref. contains greater than 10% dissolved oxygen and the partial pressure of CO₂ in the broth is pref. less than 0.04.

USE/ADVANTAGE - The process provides a high level of growth and productivity over an extended period of time. In particular, xanthophylls can be produced at levels of at least 20 mg/l/hr. The xanthophylls are useful as natural colouring agents, esp. as feed supplements for poultry. Dwg.0/0

L81 ANSWER 16 OF 17 WPIX COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: 1974-80388V [46] WPIX

TITLE: Deep culturing microorganisms with adequate

oxygen - stirring rate and
oxygen flow adjusted to secure full
oxygen access.

DERWENT CLASS: D16
PATENT ASSIGNEE(S): (KRIK-N) KIRKHENSHEIN MICROBIOL
COUNTRY COUNT: 1
PATENT INFORMATION:

| PATENT NO | KIND | DATE | WEEK | LA | PG |
|-----------|------|----------|-----------|----|----|
| SU 413183 | A | 19740528 | (197446)* | | |

PRIORITY APPLN. INFO: SU 1971-1684597 19710727

AN 1974-80388V [46] WPIX

AB SU 413183 A UPAB: 19930831

In the title **culturing** when the air input is 0.3-3.0 vols/vol. medium per min., the stirring rate is increased in steps, and when the exit gas inhibiting CO₂ concn. is 3-11% the stirring rate is cut stepwise with increase also in air supply. In the case of the lysin producer *Brevibacterium* sp. 22, at an air speed 1.2 vols/vol. medium/per min., the stirring rate steps are 180, 230, 280, 330, 380 r.p.m., and when the exit gas CO₂ conc. is 4% the stirrer speed sequence is reversed. With the **carotenoid producer** *Rhodotorula gracilis* Mn, using an air input of 2.0 vols./vol./min., the stirring speeds are 200, 300, 400 r.p.m., then with 11% CO₂ in the exit gas the sequence is reversed.

L81 ANSWER 17 OF 17 WPIX COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: 1972-39521T [25] WPIX

TITLE: **Carotenoid contg concentrates - microbiological prodn.**

DERWENT CLASS: B04 D16

PATENT ASSIGNEE(S): (KIR-N) INST MIKROBIOLOGII IM AUG

COUNTRY COUNT: 4

PATENT INFORMATION:

| PATENT NO | KIND | DATE | WEEK | LA | PG |
|-------------|------|----------|-----------|----|----|
| DE 2059387 | A | | (197225)* | | |
| GB 1293995 | A | | (197243) | | |
| FR 2117801 | A | | (197246) | | |
| JP 49004386 | B | 19740131 | (197409) | | |

PRIORITY APPLN. INFO: DE 1970-2059387 19701202

AN 1972-39521T [25] WPIX

AB DE 2059387 A UPAB: 19930831

Carotenoid-contg. concentrates useful in the prodn. of fodder prods. and in the food and medicinal inds. are produced by cultivating **carotenoid**-producing micro-organisms under aerobic conditions on a nutrient medium contg. sources of C, N, mineral salts, biologically active substances, stimulants and **carotenoid** precursors until maximal accumulation of the biomass in the **fermentation** medium, effecting a partial separation of the **fermentation** medium from the biomass to give a biomass conc. of is not <50 g (dry wt) per litre of medium, and accumulating **carotenoid** by maintaining the concentrate (optionally after adding carbohydrate and/or trace elements) at 28-35 degrees C and pH 5-7 while aerating at a rate of 80-150 mg

MARX 09/049,228

.02/litre/minute. Fermentati n time is shortened energy requirements are reduced, and the capacity and amt. of equipment required are less.

=> file home

FILE 'HOME' ENTERED AT 12:10:41 ON 28 JUL 2003

MARX 09/049,228

=> d his

(FILE 'HOME' ENTERED AT 10:50:39 ON 28 JUL 2003)

FILE 'HCAPLUS' ENTERED AT 10:50:50 ON 28 JUL 2003.

L1 19 S TSUBOKURA A?/AU
 L2 337 S MIZUTA H?/AU
 L3 354 S L1-2
 L4 8 S L3 AND CAROTENOID
 SELECT RN L4 1-8

FILE 'REGISTRY' ENTERED AT 10:51:40 ON 28 JUL 2003

L5 42 S E1-42
 SAVE TEMP L5 MAR228INV/A

FILE 'HCAPLUS' ENTERED AT 10:51:59 ON 28 JUL 2003

L6 5 S L4 AND L5
 L7 8 S L4 OR L6 *8 cites w/ 42 cpds displayed*

=> d ibib abs hitstr ind 1-8

L7 ANSWER 1 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:924027 HCAPLUS
 DOCUMENT NUMBER: 136:52783
 TITLE: Process for producing carotenoid pigments
 INVENTOR(S): Tsubokura, Akira; Mizuta, Haruyoshi
 PATENT ASSIGNEE(S): Nippon Mitsubishi Oil Corporation, Japan
 SOURCE: PCT Int. Appl., 23 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: Japanese
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|--|------|----------|-----------------|----------|
| WO 2001096591 | A1 | 20011220 | WO 2001-JP4874 | 20010608 |
| W: AU, CA, CN, IL, KR, US RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR | | | | |
| JP 2001352995 | A2 | 20011225 | JP 2000-175124 | 20000612 |
| AU 2001062730 | A5 | 20011224 | AU 2001-62730 | 20010608 |
| EP 1229126 | A1 | 20020807 | EP 2001-936932 | 20010608 |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY, TR | | | | |
| US 2003044886 | A1 | 20030306 | US 2002-49228 | 20020211 |
| PRIORITY APPLN. INFO.: JP 2000-175124 A 20000612 WO 2001-JP4874 W 20010608 | | | | |

AB A process for the microbial manuf. of carotenoids of desired ratio of carotenoid compds. with bacteria E-396 and A-581-1 which have low growth rate and enable easy isolation of the carotenoids was given: The ratio of the carotenoid compds. (i.e., astaxanthin, adonixanthin, .beta.-carotene, echinenone, canthaxanthin, zeaxanthin, .beta.-cryptoxanthin, 3-hydroxyechinenone, adonirubin, etc.) is controlled by the concn. of oxygen dissolved in a liq. culture medium during the fermn.

IT 382660-64-2 382660-65-3
 RL: PRP (Properties)
 (nucleotide sequence; process for producing carotenoid pigments)

MARX 09/049,228

RN 382660-64-2 HCAPLUS
CN DNA (bacteria strain E-396 16S ribosomal RNA gene plus flanks) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

RN 382660-65-3 HCAPLUS
CN DNA (bacteria strain A-581-1 16S ribosomal RNA gene plus flanks) (9CI) (CA INDEX NAME)

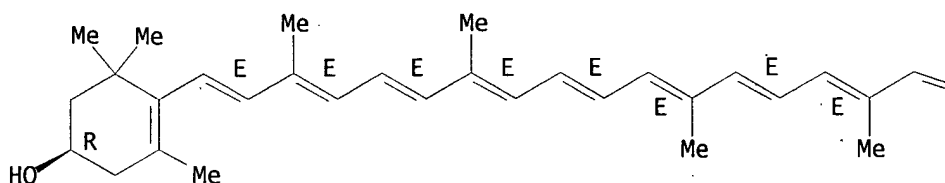
*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

IT 144-68-3P, Zeaxanthin 432-68-8P, Echinenone
472-61-7P, Astaxanthin 472-70-8P, .beta.-Cryptoxanthin
514-78-3P, Canthaxanthin 4339-77-9P, 3-Hydroxyechinenone
4418-72-8P, Adonirubin 4418-73-9P, Adonixanthin
7235-40-7P, .beta.-Carotene
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(process for producing carotenoid pigments)

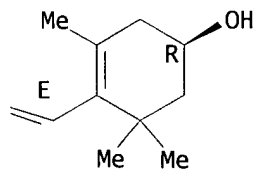
RN 144-68-3 HCAPLUS
CN .beta.,.beta.-Carotene-3,3'-diol, (3R,3'R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



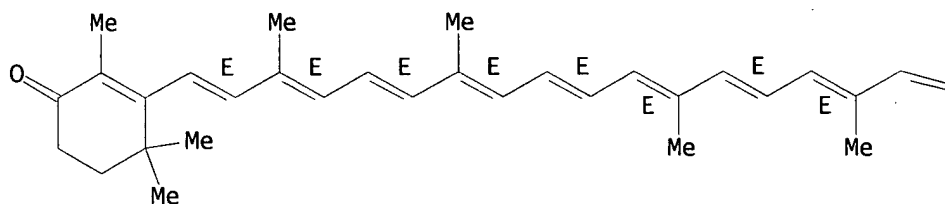
PAGE 1-B



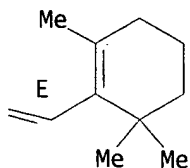
RN 432-68-8 HCAPLUS
CN .beta.,.beta.-Caroten-4-one (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

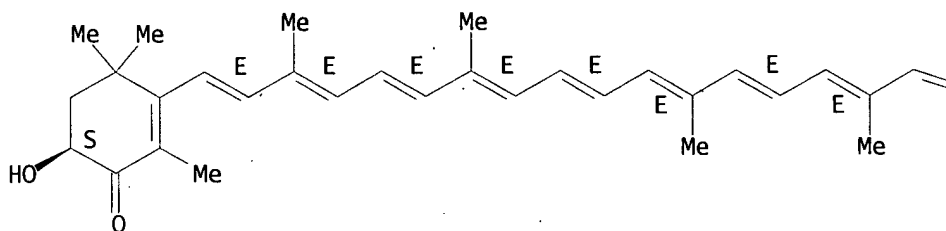


RN 472-61-7 HCAPLUS

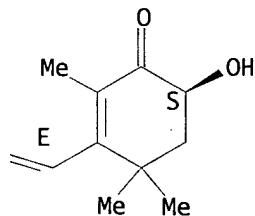
CN .beta.,.beta.-Carotene-4,4'-dione, 3,3'-dihydroxy-, (3S,3'S)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

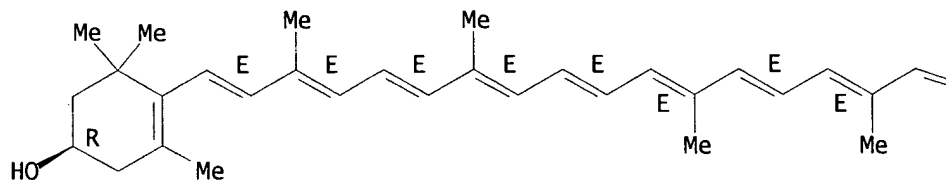


RN 472-70-8 HCAPLUS

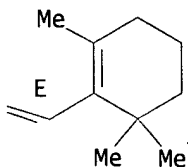
CN .beta.,.beta.-Caroten-3-ol, (3R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



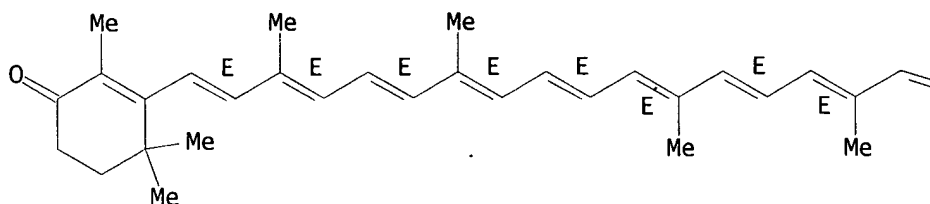
PAGE 1-B



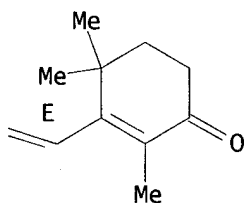
RN 514-78-3 HCAPLUS
CN .beta.,.beta.-Carotene-4,4'-dione (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



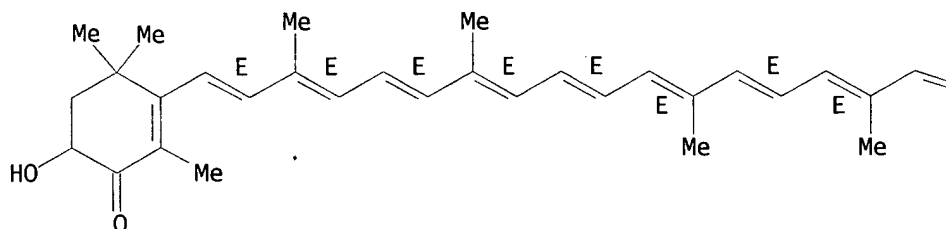
PAGE 1-B



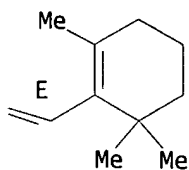
RN 4339-77-9 HCAPLUS
CN .beta.,.beta.-Caroten-4-one, 3-hydroxy- (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

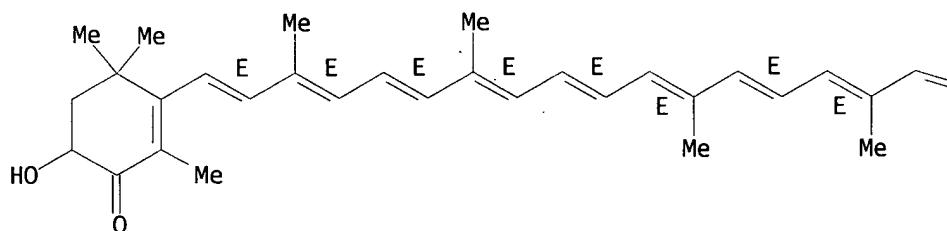


RN 4418-72-8 HCAPLUS

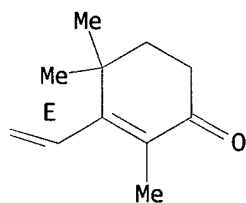
CN .beta.,.beta.-Carotene-4,4'-dione, 3-hydroxy- (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

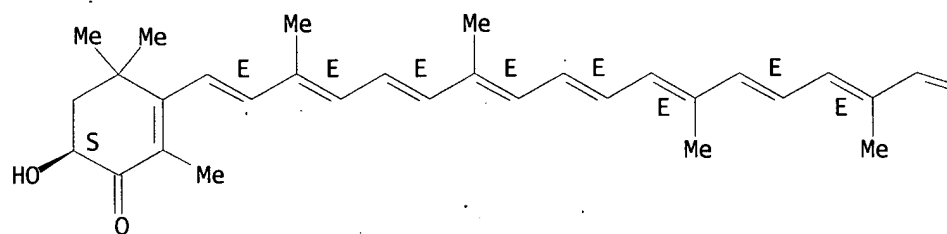


RN 4418-73-9 HCAPLUS

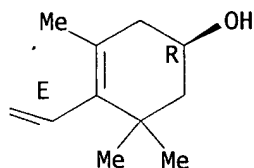
CN .beta.,.beta.-Caroten-4-one, 3,3'-dihydroxy-, (3S,3'R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



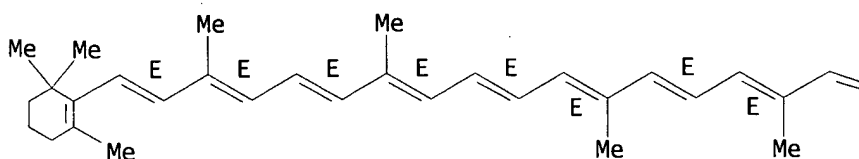
PAGE 1-B



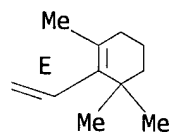
RN 7235-40-7 HCAPLUS
 CN .beta.,.beta.-Carotene (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B



IT 7782-44-7, Oxygen, biological studies
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (process for producing **carotenoid** pigments)
 RN 7782-44-7 HCAPLUS
 CN Oxygen (8CI, 9CI) (CA INDEX NAME)

O=O

IC ICM C12P023-00
 CC 16-2 (Fermentation and Bioindustrial Chemistry)
 ST **carotenoid** manuf bacteria dissolved oxygen
 IT rRNA
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (16 S, gene for; process for producing **carotenoid** pigments)
 IT Bacteria (Eubacteria)
 Culture media
 DNA sequences
 Fermentation
 Taxonomy
 (process for producing **carotenoid** pigments)
 IT Carotenes, preparation
 RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP
 (Preparation)
 (process for producing **car tenoid** pigments)
 IT Gene, microbial

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(process for producing **carotenoid** pigments)

IT 382660-64-2 382660-65-3

RL: PRP (Properties)
(nucleotide sequence; process for producing **carotenoid** pigments)

IT 144-68-3P, Zeaxanthin 432-68-8P, Echinenone
472-61-7P, Astaxanthin 472-70-8P, .beta.-Cryptoxanthin
514-78-3P, Canthaxanthin 4339-77-9P, 3-Hydroxyechinenone
4418-72-8P, Adonirubin 4418-73-9P, Adonixanthin
7235-40-7P, .beta.-Carotene

RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(process for producing **carotenoid** pigments)

IT 7782-44-7, Oxygen, biological studies

RL: BSU (Biological study, unclassified); BIOL (Biological study)
(process for producing **carotenoid** pigments)

REFERENCE COUNT: 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 2 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:251697 HCAPLUS

DOCUMENT NUMBER: 134:294933

TITLE: Bacterial **carotenoid**-containing preparations as feed additive

INVENTOR(S): Tsubokura, Akira; Yoneda, Hisashi; Mizuta, Yoshinori

PATENT ASSIGNEE(S): Nisseki Mitsubishi K. K., Japan

SOURCE: Jpn. Kokai Tokkyo Koho, 6 pp.

CODEN: JKXXAF

DOCUMENT TYPE: Patent

LANGUAGE: Japanese

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------------------------|------|----------|------------------|----------|
| JP 2001095500 | A2 | 20010410 | JP 1999-279337 | 19990930 |
| NO 2001002629 | A | 20010711 | NO 2001-2629 | 20010529 |
| PRIORITY APPLN. INFO.: | | | JP 1999-279337 A | 19990930 |
| | | | WO 2000-JP6528 W | 20000922 |

AB The preps. comprise ppt. of microbial culture contg. .gtoreq.3% **carotenoids** with astaxanthin content preferably .gtoreq.40%. The microbes are preferably those which contain 16 S rRNA-specifying DNA having sequence substantially homologous to 1452-bp sequence (given). The **carotenoids** are stable to O and light because they are stabilized with cell membrane and cell wall. E-396 (FERM BP-4283) was cultured in a medium contg. yeast ext., peptone, glucose, and salts at 28.degree. for 6 days. The collected cells was dried to give a pigment prepn. (total **carotenoids** 31.2%) contg. .beta.-carotene 1.6, echinenone 1.9, 3-hydroxyechinenone 0.9, canthaxanthin 2.3, adonirubin 5.6, astaxanthin 13.0, asteroideone 0.6, adonixanthin 5.3, and zeaxanthin 0.01%.

IT 144-68-3P, Zeaxanthin 432-68-8P, Echinenone
472-61-7P, Astaxanthin 514-78-3P, Canthaxanthin
4339-77-9P, 3-Hydroxyechinenone 4418-72-8P, Adonirubin
4418-73-9P, Adonixanthin 7235-40-7P, .beta.-Carotene
19866-02-5P, Asteroideone

RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); FFD (Food or feed use); BIOL (Biological study); PREP (Preparation); USES

(Uses)

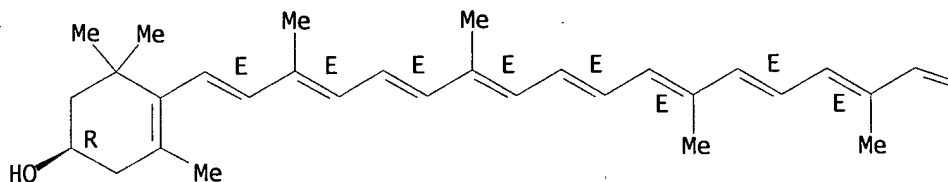
(manuf. of astaxanthin-rich carotenoid-contg. preps. for
feed with microorganisms having specific 16 S rRNA-specifying DNA
sequence)

RN 144-68-3 HCAPLUS

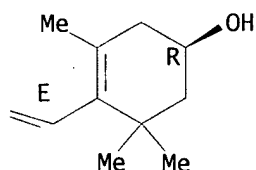
CN .beta.,.beta.-Carotene-3,3'-diol, (3R,3'R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

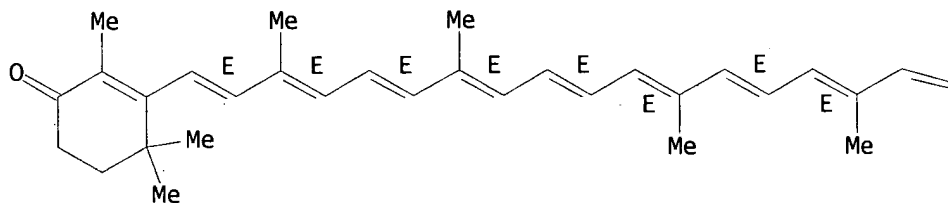


RN 432-68-8 HCAPLUS

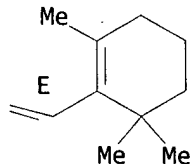
CN .beta.,.beta.-Caroten-4-one (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

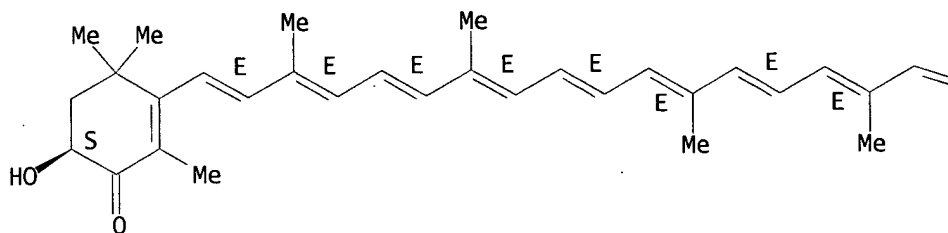


RN 472-61-7 HCAPLUS

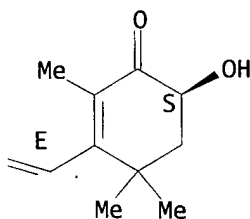
CN .beta.,.beta.-Carotene-4,4'-dione, 3,3'-dihydroxy-, (3S,3'S)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



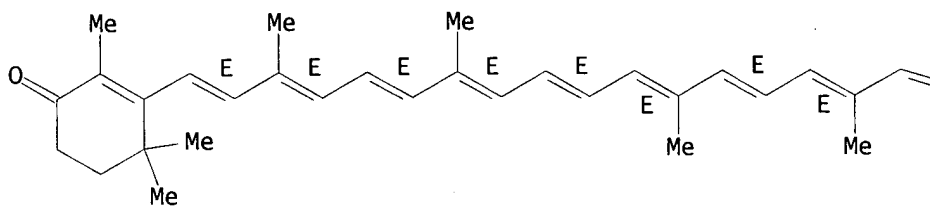
PAGE 1-B



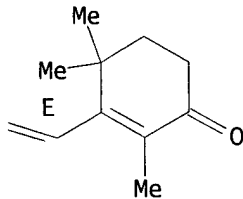
RN 514-78-3 HCAPLUS
CN .beta.,.beta.-Carotene-4,4'-dione (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



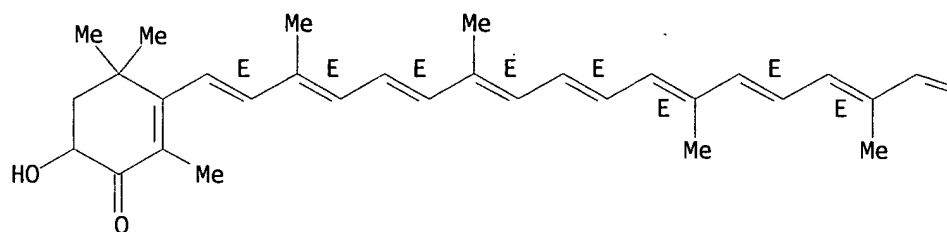
PAGE 1-B



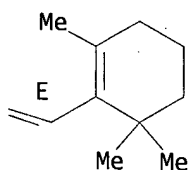
RN 4339-77-9 HCAPLUS
CN .beta.,.beta.-Caroten-4-one, 3-hydroxy- (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

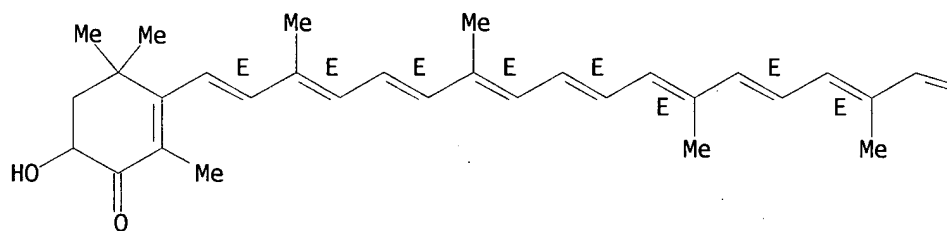


RN 4418-72-8 HCAPLUS

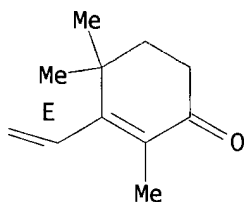
CN .beta.,.beta.-Carotene-4,4'-dione, 3-hydroxy- (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

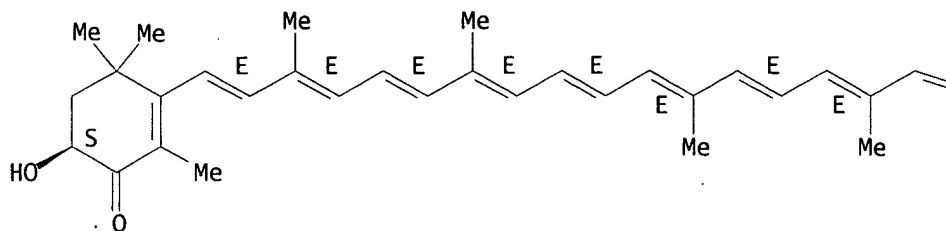


RN 4418-73-9 HCAPLUS

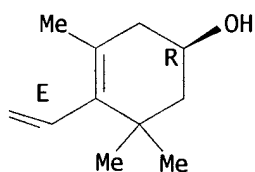
CN .beta.,.beta.-Caroten-4-one, 3,3'-dihydroxy-, (3S,3'R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



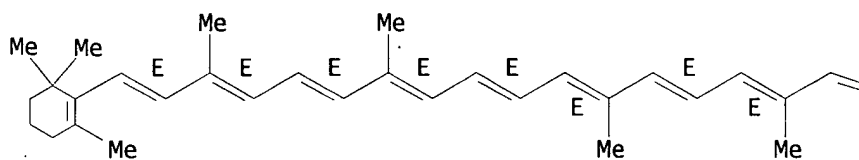
PAGE 1-B



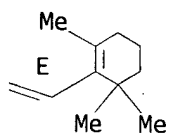
RN 7235-40-7 HCAPLUS
 CN .beta.,.beta.-Carotene (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



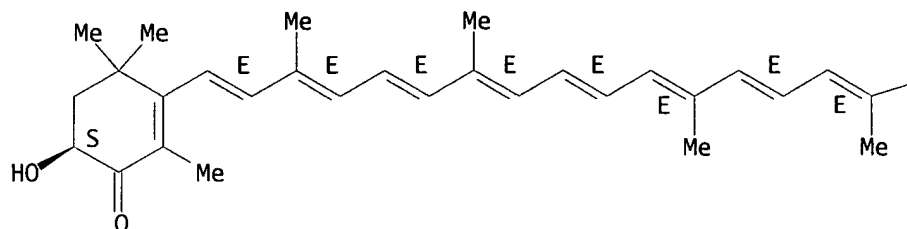
PAGE 1-B



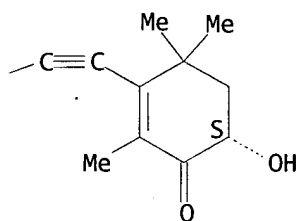
RN 19866-02-5 HCAPLUS
 CN .beta.,.beta.-Carotene-4,4'-dione, 7,8-didehydro-3,3'-dihydroxy-,
 (3S,3'S)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
 Double bond geometry as shown.

PAGE 1-A



PAGE 1-B



IT 334071-56-6

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(manuf. of astaxanthin-rich **carotenoid**-contg. prepns. for feed with microorganisms having specific 16 S rRNA-specifying DNA sequence)

RN 334071-56-6 HCAPLUS

CN DNA (bacteria strain E-396 16 S rRNA gene) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

IC ICM A23K001-16

ICS C09B061-00; C09B067-20; C12N001-20

CC 17-12 (Food and Feed Chemistry)

Section cross-reference(s): 16, 18

ST astaxanthin rich **carotenoid** contg microbial culture feed additive

IT rRNA

RL: BSU (Biological study, unclassified); BIOL (Biological study)

(16 S, DNA for; manuf. of astaxanthin-rich **carotenoid**-contg.

prepns. for feed with microorganisms having specific 16 S

rRNA-specifying DNA sequence)

IT Bacteria (Eubacteria)

(E-396; manuf. of astaxanthin-rich **carotenoid**-contg. prepns.

for feed with microorganisms having specific 16 S rRNA-specifying DNA sequence)

IT Feed additives

Fermentation

Pigments, biological

(manuf. of astaxanthin-rich **carotenoid**-contg. prepns. for

feed with microorganisms having specific 16 S rRNA-specifying DNA sequence)

IT Carotenes, biological studies

RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); FFD

(Food or feed use); BIOL (Biological study); PREP (Preparation); USES

(Uses)

(manuf. of astaxanthin-rich **carotenoid**-contg. prepns. for

feed with microorganisms having specific 16 S rRNA-specifying DNA sequence)

IT DNA

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(manuf. of astaxanthin-rich **carotenoid**-contg. prepns. for feed with microorganisms having specific 16 S rRNA-specifying DNA sequence)

IT 144-68-3P, Zeaxanthin 432-68-8P, Echinenone

472-61-7P, Astaxanthin 514-78-3P, Canthaxanthin

4339-77-9P, 3-Hydroxyechinenone 4418-72-8P, Adonirubin

4418-73-9P, Adonixanthin 7235-40-7P, .beta.-Carotene

19866-02-5P, Asteroidenone

RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); FFD (Food or feed use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(manuf. of astaxanthin-rich **carotenoid**-contg. prepns. for feed with microorganisms having specific 16 S rRNA-specifying DNA sequence)

IT 334071-56-6

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(manuf. of astaxanthin-rich **carotenoid**-contg. prepns. for feed with microorganisms having specific 16 S rRNA-specifying DNA sequence)

L7 ANSWER 3 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1999:85961 HCAPLUS

DOCUMENT NUMBER: 130:279042

TITLE: Paracoccus carotinifaciens sp. nov., a new aerobic gram-negative astaxanthin-producing bacterium

AUTHOR(S): Tsubokura, Akira; Yoneda, Hisashi; Mizuta, Haruyoshi

CORPORATE SOURCE: Central Technical Research Laboratory, Nippon Oil Company Ltd, Yokohama, 231-0815, Japan

SOURCE: International Journal of Systematic Bacteriology (1999), 49(1), 277-282

CODEN: IJSBA8; ISSN: 0020-7713

PUBLISHER: Society for General Microbiology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The strain E-396T, isolated from soil, was Gram-neg., aerobic, orange-pigmented, rod-shaped, motile by peritrichous flagella and astaxanthin-producing. This organism produced **carotenoids**, mainly astaxanthin, and did not produce bacteriochlorophyll. The ubiquinone system was Q-10. Anal. of the 16S rRNA sequence of strain E-396T showed it to be a member of the .alpha.-3 subclass of the Proteobacteria, forming a cluster with the species of the genus Paracoccus. On the basis of the prodn. of orange pigments and motility by peritrichous flagella, together with DNA-DNA reassocn. data, it is concluded that the new isolate should be classified into a new species of the genus Paracoccus, Paracoccus carotinifaciens sp. nov. The type strain is E-396T (= IFO 16121T).

IT 472-61-7, Astaxanthin

RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)

(Paracoccus carotinifaciens sp. nov., new aerobic gram-neg. astaxanthin-producing bacterium)

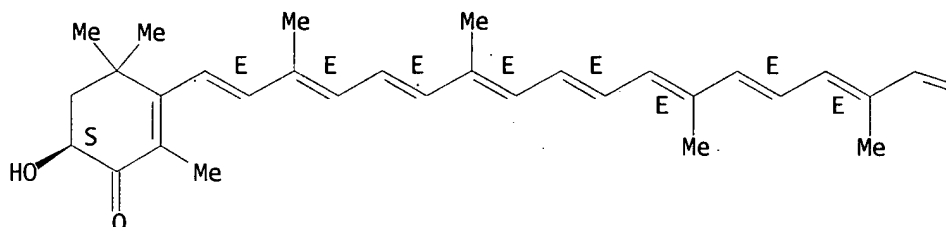
RN 472-61-7 HCAPLUS

CN .beta.,.beta.-Carotene-4,4'-dione, 3,3'-dihydroxy-, (3S,3'S)- (9CI) (CA

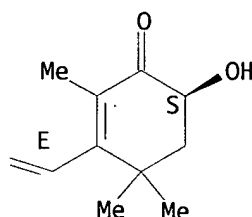
INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



PAGE 1-B



IT 222713-29-3

RL: PRP (Properties)

(nucleotide sequence; *Paracoccus carotinifaciens* sp. nov., new aerobic gram-neg. astaxanthin-producing bacterium)

RN 222713-29-3 HCAPLUS

CN DNA (*Paracoccus carotinifaciens* strain E-396 16S rRNA gene) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

CC 10-1 (Microbial, Algal, and Fungal Biochemistry)

Section cross-reference(s): 3

ST *Paracoccus carotinifaciens* 16S rRNA gene sequence taxonomy

IT rRNA

RL: PRP (Properties)

(16 S; *Paracoccus carotinifaciens* sp. nov., new aerobic gram-neg. astaxanthin-producing bacterium)

IT DNA sequences

Evolution

Paracoccus carotinifaciens

Taxonomy

(*Paracoccus carotinifaciens* sp. nov., new aerobic gram-neg. astaxanthin-producing bacterium)

IT Gene, microbial

RL: PRP (Properties)

(for 16S rRNA; *Paracoccus carotinifaciens* sp. nov., new aerobic gram-neg. astaxanthin-producing bacterium)

IT 472-61-7, Astaxanthin

RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)

(*Paracoccus carotinifaciens* sp. nov., new aerobic gram-neg.
astaxanthin-producing bacterium)

IT 222713-29-3

RL: PRP (Properties)

(nucleotide sequence; *Paracoccus carotinifaciens* sp. nov., new aerobic
gram-neg. astaxanthin-producing bacterium)

REFERENCE COUNT: 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 4 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1997:772393 HCAPLUS

DOCUMENT NUMBER: 128:59314

TITLE: Carotenoid-stabilization material

INVENTOR(S): Tsubokura, Akira; Yoneda, Hisashi; Uchiyama,
Yoko; Mizuta, Yoshitaka

PATENT ASSIGNEE(S): Nippon Oil Co., Ltd., Japan

SOURCE: Jpn. Kokai Tokkyo Koho, 14 pp.

CODEN: JKXXAF

DOCUMENT TYPE: Patent

LANGUAGE: Japanese

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|-------------|------|----------|-----------------|----------|
| JP 09308481 | A2 | 19971202 | JP 1996-128565 | 19960523 |
| JP 3278574 | B2 | 20020430 | | |

PRIORITY APPLN. INFO.: JP 1996-128565 19960523

AB The title material (I) is produced by microorganism E-396 or mutant
microorganism A-581-1. I is useful for improvement/stabilization of meat,
egg, and/or skin color. Physiol. and morphol. characteristics of the
microorganism E-396 were given.

IC ICM C12N001-20

ICS A23K001-16; A23K001-18; A23L001-272; C09B061-00; C12N015-09;
C12Q001-68; C12N001-20; C12R001-01

CC 10-1 (Microbial, Algal, and Fungal Biochemistry)

Section cross-reference(s): 16, 17

ST carotenoid stabilization material microorganism fermn

IT Aquaculture

Egg, poultry

Feed additives

Fermentation

Food additives

Health food

Meat

Microorganism

(carotenoid-stabilization material)

IT Carotenes, biological studies

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL
(Biological study); PROC (Process)

(carotenoid-stabilization material)

L7 ANSWER 5 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1996:338419 HCAPLUS

DOCUMENT NUMBER: 125:9229

TITLE: Process for extraction of carotenoids from
bacterial cellsINVENTOR(S): Kitaoka, Motomitsu; Tsubokura, Akira;
Kiyota, Takashi

PATENT ASSIGNEE(S): Nippon Oil Company, Ltd., Japan

SOURCE: Can. Pat. Appl., 10 pp.
 CODEN: CPXXEB
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|-------------|------|----------|-----------------|----------|
| CA 2159176 | AA | 19960328 | CA 1995-2159176 | 19950926 |
| JP 08089280 | A2 | 19960409 | JP 1994-231266 | 19940927 |
| US 5591343 | A | 19970107 | US 1995-533390 | 19950925 |
| NO 9503813 | A | 19960328 | NO 1995-3813 | 19950926 |
| EP 719866 | A1 | 19960703 | EP 1995-306770 | 19950926 |
| EP 719866 | B1 | 20011205 | | |

R: CH, DE, FR, GB, LI

PRIORITY APPLN. INFO.: JP 1994-231266 A 19940927

AB A process for extn. of a **carotenoid** compd. from bacterial cells contg. the **carotenoid** compd. comprising the step of bringing the bacterial cells into contact with supercrit. fluid to ext. the **carotenoid** compd. from the cells. The process provides **carotenoid** compds. which can be safely used as feed additives and food additives.

IC ICM C07C403-00

ICS C07C011-21

CC 17-14 (Food and Feed Chemistry)

ST process extn **carotenoid** bacterial cell

IT Feed

Food

(additives; process for extn. of **carotenoids** from bacterial cells)

IT Bacteria

Extraction

(process for extn. of **carotenoids** from bacterial cells)

IT Carotenes and **Carotenoids**, biological studies

RL: FFD (Food or feed use); PUR (Purification or recovery); BIOL (Biological study); PREP (Preparation); USES (Uses)

(process for extn. of **carotenoids** from bacterial cells)

IT Fluids

(supercrit., process for extn. of **carotenoids** from bacterial cells)

L7 ANSWER 6 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1996:153672 HCAPLUS

DOCUMENT NUMBER: 124:198044

TITLE: Novel bacteria producing **carotenoids**

INVENTOR(S): Tsubokura, Akira; Yoneda, Hisashi; Takagi, Mikihiro; Kyota, Takashi

PATENT ASSIGNEE(S): Nippon Oil Co Ltd, Japan

SOURCE: Jpn. Kokai Tokkyo Koho, 20 pp.

CODEN: JKXXAF

DOCUMENT TYPE: Patent

LANGUAGE: Japanese

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|-------------|------|----------|-----------------|----------|
| JP 08009964 | A2 | 19960116 | JP 1994-152078 | 19940704 |
| JP 3429563 | B2 | 20030722 | | |

PRIORITY APPLN. INFO.: JP 1994-152078 19940704
 AB Two novel bacteria capable of producing **carotenoids** are isolated and characterized. FERM BP-4283 strain E-396 and FERM BP-4671 strain A-581-1 are both aerobic, gram-neg. bacteria. A phylogenetic tree of the bacteria is also provided.
 IC ICM C12N001-20
 ICA C12P023-00
 ICI C12N001-20, C12R001-01; C12P023-00, C12R001-01
 CC 10-1 (Microbial, Algal, and Fungal Biochemistry)
 ST bacteria **carotenoid** prodn
 IT Bacteria
 (FERM BP-4283 strain E-396, FERM BP-4671 strain A-581-1; isolation of novel bacteria producing **carotenoids**)
 IT Carotenes and **Carotenoids**, preparation
 RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
 (isolation of novel bacteria producing **carotenoids**)

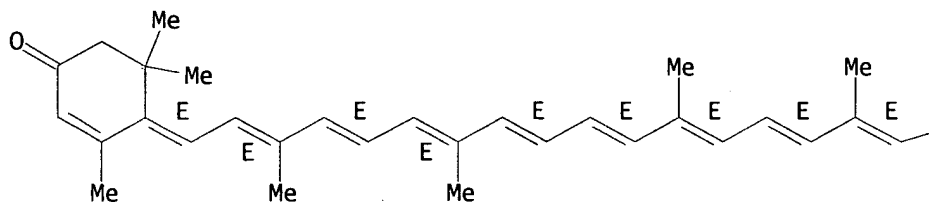
L7 ANSWER 7 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN
 ACCESSION NUMBER: 1995:849314 HCAPLUS
 DOCUMENT NUMBER: 123:254690
 TITLE: Process for extracting **carotenoids**
 INVENTOR(S): Kitaoka, Motomitsu; Tsubokura, Akira;
 Kiyota, Takashi
 PATENT ASSIGNEE(S): Nippon Oil Co. Ltd., Japan
 SOURCE: Eur. Pat. Appl., 10 pp.
 CODEN: EPXXDW
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------------------------|------|----------|-----------------|----------|
| EP 670306 | A1 | 19950906 | EP 1995-102933 | 19950302 |
| R: CH, DE, FR, GB, LI | | | | |
| JP 07242621 | A2 | 19950919 | JP 1994-32388 | 19940302 |
| CA 2143689 | AA | 19950903 | CA 1995-2143689 | 19950301 |
| NO 9500804 | A | 19950904 | NO 1995-804 | 19950301 |
| PRIORITY APPLN. INFO.: | | | JP 1994-32388 | 19940302 |

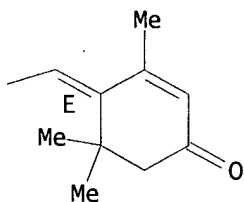
AB A process for extg. **carotenoid** compds. comprising the step of bringing a material contg. the **carotenoid** compd. into contact with a cyclic hydrophilic org. compd. to ext. the **carotenoid** compd. from the material to the cyclic hydrophilic org. compd. By this process, a **carotenoid** compd. can be efficiently extd. resulting in an ext. contg. a high concn. of the **carotenoid** compd.
 IT **116-30-3P 144-68-3P, Zeaxanthin 432-68-8P, Echinenone 432-70-2P, .alpha.-Carotene 472-61-7P, Astaxanthin 472-70-8P, Cryptoxanthin 472-93-5P, .gamma.-Carotene 502-65-8P, Lycopene 514-78-3P, Canthaxanthin 4339-77-9P, 3-Hydroxyechinenone 4418-72-8P, Adonirubin 4418-73-9P, Adonixanthin 7235-40-7P, .beta.-Carotene**
 RL: BMF (Bioindustrial manufacture); PUR (Purification or recovery); BIOL (Biological study); PREP (Preparation)
 (extg. **carotenoids**)
 RN 116-30-3 HCAPLUS
 CN 4,5'-retro-.beta.,.beta.-Carotene-3,3'-dione, 4',5'-didehydro- (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

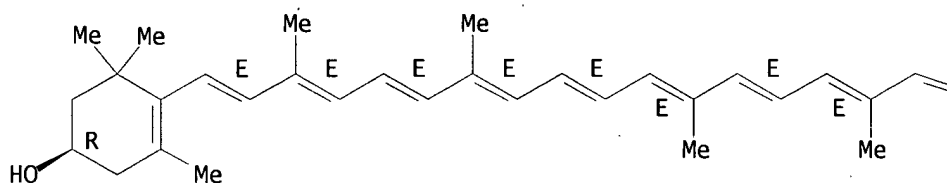


RN 144-68-3 HCAPLUS

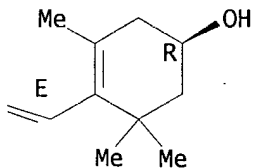
CN .beta.,.beta.-Carotene-3,3'-diol, (3R,3'R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

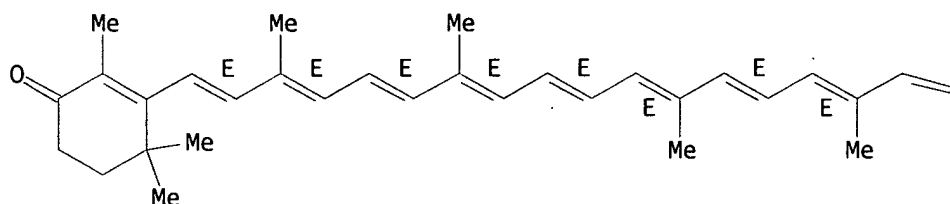


RN 432-68-8 HCAPLUS

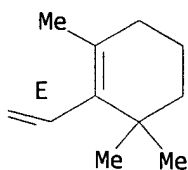
CN .beta.,.beta.-Caroten-4-one (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



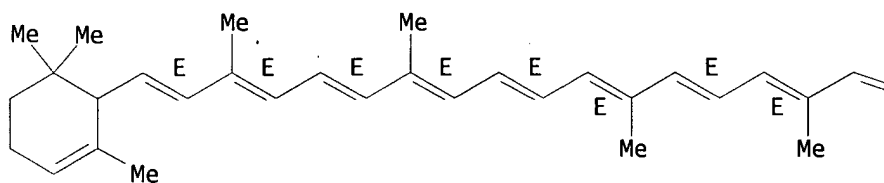
PAGE 1-B



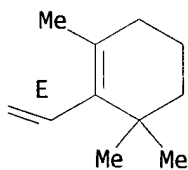
RN 432-70-2 HCAPLUS
 CN .beta.,.epsilon.-Carotene (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



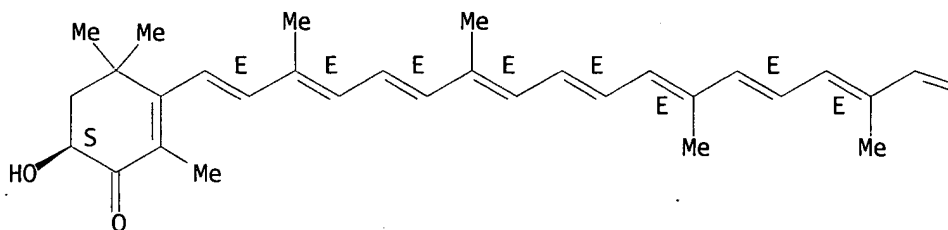
PAGE 1-B



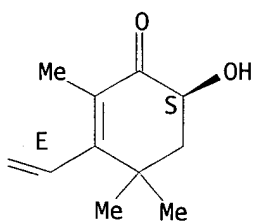
RN 472-61-7 HCAPLUS
 CN .beta.,.beta.-Carotene-4,4'-dione, 3,3'-dihydroxy-, (3S,3'S)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
 Double bond geometry as shown.

PAGE 1-A



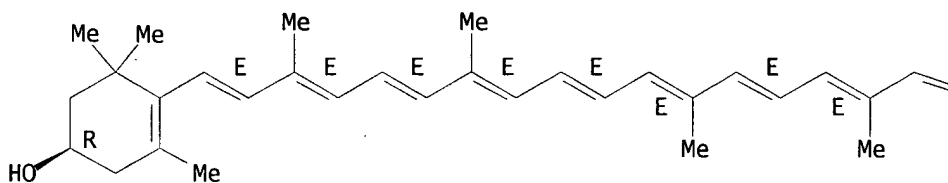
PAGE 1-B



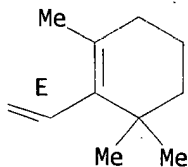
RN 472-70-8 HCAPLUS
 CN .beta.,.beta.-Caroten-3-ol, (3R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
 Double bond geometry as shown.

PAGE 1-A



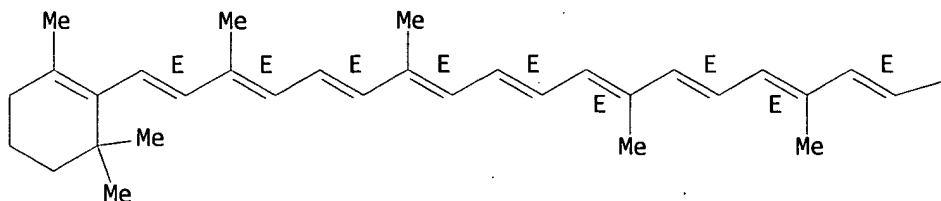
PAGE 1-B



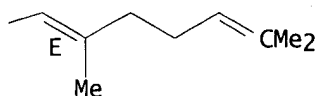
RN 472-93-5 HCAPLUS
 CN .beta.,.psi.-Carotene (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



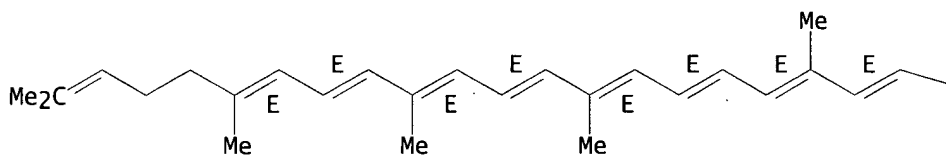
PAGE 1-B



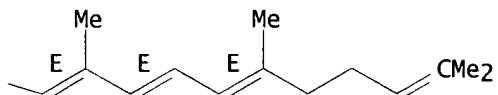
RN 502-65-8 HCAPLUS
 CN .psi.,.psi.-Carotene (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



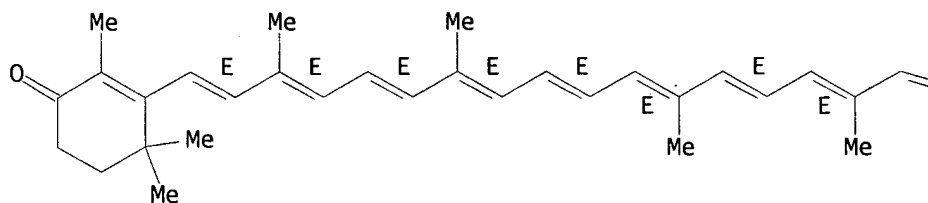
PAGE 1-B



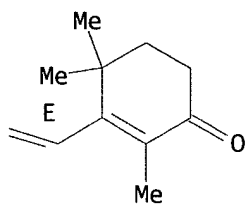
RN 514-78-3 HCAPLUS
 CN .beta.,.beta.-Carotene-4,4'-dione (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

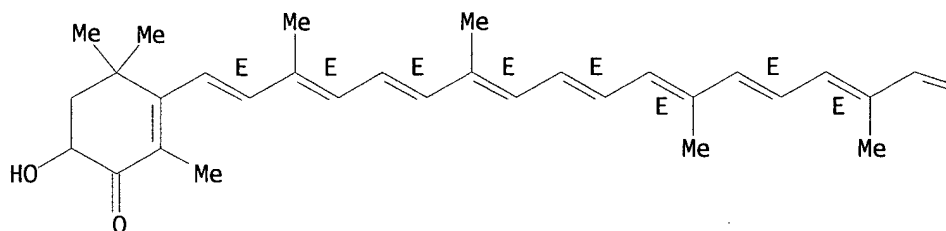


RN 4339-77-9 HCAPLUS

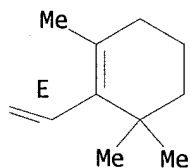
CN .beta.,.beta.-Caroten-4-one, 3-hydroxy- (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

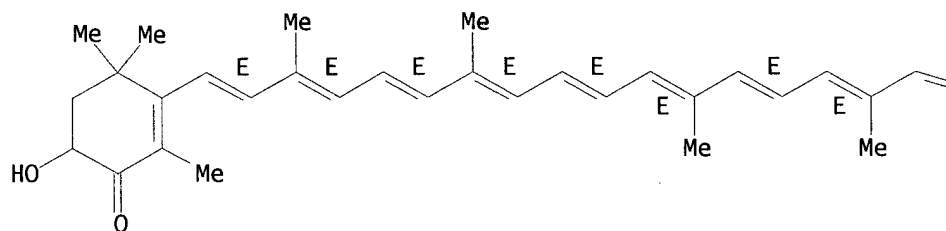


RN 4418-72-8 HCAPLUS

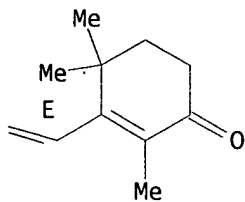
CN .beta.,.beta.-Carotene-4,4'-dione, 3-hydroxy- (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

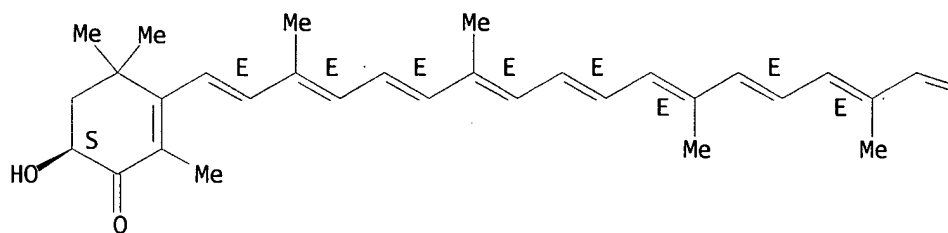


RN 4418-73-9 HCAPLUS

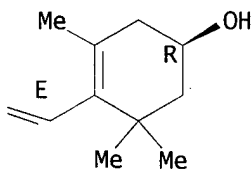
CN .beta.,.beta.-Caroten-4-one, 3,3'-dihydroxy-, (3S,3'R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

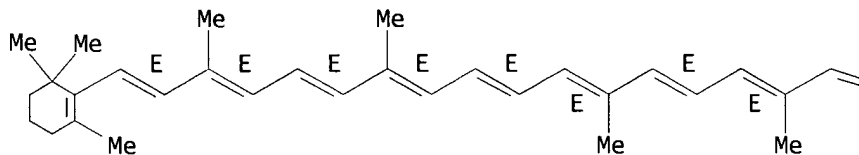


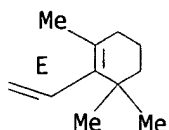
RN 7235-40-7 HCAPLUS

CN .beta.,.beta.-Carotene (9CI) (CA INDEX NAME)

Double bond geometry as shown.

PAGE 1-A



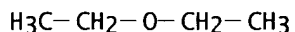


IT 60-29-7, Diethyl ether, uses 64-17-5, Ethanol, uses 67-56-1, Methanol, uses 67-64-1, Acetone, uses 67-66-3, Chloroform, uses 71-23-8, Propanol, uses 71-43-2, Benzene, uses 75-09-2, Dichloromethane, uses 78-93-3, Methyl ethyl ketone, uses 108-20-3, Isopropyl ether 108-88-3, Toluene, uses 108-94-1, Cyclohexanone, uses 109-99-9, THF, uses 110-54-3, Hexane, uses 110-82-7, Cyclohexane, uses 110-86-1, Pyridine, uses 123-86-4, Butyl acetate 123-91-1, Dioxane, uses 141-78-6, Ethyl acetate, uses 142-82-5, Heptane, uses 563-80-4, Methyl isopropyl ketone 1330-20-7, Xylene, uses

RL: NUU (Other use, unclassified); USES (Uses)
(extg. **carotenoids**)

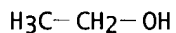
RN 60-29-7 HCAPLUS

CN Ethane, 1,1'-oxybis- (9CI) (CA INDEX NAME)



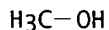
RN 64-17-5 HCAPLUS

CN Ethanol (9CI) (CA INDEX NAME)



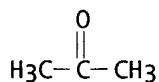
RN 67-56-1 HCAPLUS

CN Methanol (8CI, 9CI) (CA INDEX NAME)



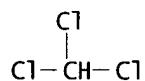
RN 67-64-1 HCAPLUS

CN 2-Propanone (9CI) (CA INDEX NAME)

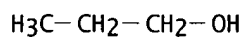


RN 67-66-3 HCAPLUS

CN Methane, trichloro- (9CI) (CA INDEX NAME)



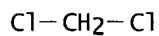
RN 71-23-8 HCAPLUS
CN 1-Propanol (9CI) (CA INDEX NAME)



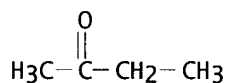
RN 71-43-2 HCAPLUS
CN Benzene (8CI, 9CI) (CA INDEX NAME)



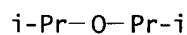
RN 75-09-2 HCAPLUS
CN Methane, dichloro- (8CI, 9CI) (CA INDEX NAME)



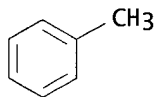
RN 78-93-3 HCAPLUS
CN 2-Butanone (8CI, 9CI) (CA INDEX NAME)



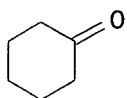
RN 108-20-3 HCAPLUS
CN Propane, 2,2'-oxybis- (9CI) (CA INDEX NAME)



RN 108-88-3 HCAPLUS
CN Benzene, methyl- (9CI) (CA INDEX NAME)



RN 108-94-1 HCAPLUS
CN Cyclohexanone (7CI, 8CI, 9CI) (CA INDEX NAME)



RN 109-99-9 HCAPLUS
CN Furan, tetrahydro- (7CI, 8CI, 9CI) (CA INDEX NAME)



RN 110-54-3 HCAPLUS
CN Hexane (8CI, 9CI) (CA INDEX NAME)

Me-(CH₂)₄-Me

RN 110-82-7 HCAPLUS
CN Cyclohexane (8CI, 9CI) (CA INDEX NAME)



RN 110-86-1 HCAPLUS
CN Pyridine (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



RN 123-86-4 HCAPLUS
CN Acetic acid, butyl ester (8CI, 9CI) (CA INDEX NAME)

n-Bu-O-Ac

RN 123-91-1 HCAPLUS
CN 1,4-Dioxane (9CI) (CA INDEX NAME)



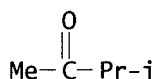
RN 141-78-6 HCAPLUS
CN Acetic acid ethyl ester (8CI, 9CI) (CA INDEX NAME)

Et-O-Ac

RN 142-82-5 HCAPLUS
 CN Heptane (8CI, 9CI) (CA INDEX NAME)

Me-(CH₂)₅-Me

RN 563-80-4 HCAPLUS
 CN 2-Butanone, 3-methyl- (8CI, 9CI) (CA INDEX NAME)



RN 1330-20-7 HCAPLUS
 CN Benzene, dimethyl- (9CI) (CA INDEX NAME)



2 (D1-Me)

IC ICM C07C403-24
 ICS C12P023-00
 CC 16-1 (Fermentation and Bioindustrial Chemistry)
 ST **carotenoid** fermn extn
 IT Algae
 Bacteria
 Corynebacterium
 Dunaliella
 Fermentation
 Haematococcus pluvialis
 Phaffia rhodozyma
 (carotenoid extn. from)
 IT Carotenes and **Carotenoids**, preparation
 RL: BMF (Bioindustrial manufacture); PUR (Purification or recovery); BIOL
 (Biological study); PREP (Preparation)
 (extg. **carotenoids**)
 IT Ligroine
 RL: NUU (Other use, unclassified); USES (Uses)
 (extg. **carotenoids**)
 IT 116-30-3P 144-68-3P, Zeaxanthin 432-68-8P,
 Echinenone 432-70-2P, .alpha.-Carotene 472-61-7P,
 Astaxanthin 472-70-8P, Cryptoxanthin 472-93-5P,
 .gamma.-Carotene 502-65-8P, Lycopene 514-78-3P,
 Canthaxanthin 4339-77-9P, 3-Hydroxyechinenone 4418-72-8P,
 , Adonirubin 4418-73-9P, Adonixanthin 7235-40-7P,
 .beta.-Carotene

RL: BMF (Bioindustrial manufacture); PUR (Purification or recovery); BIOL (Biological study); PREP (Preparation)

(extg. **carotenoids**)

IT 60-29-7, Diethyl ether, uses 64-17-5, Ethanol, uses 67-56-1, Methanol, uses 67-64-1, Acetone, uses 67-66-3, Chloroform, uses 71-23-8, Propanol, uses 71-43-2, Benzene, uses 75-09-2, Dichloromethane, uses 78-93-3, Methyl ethyl ketone, uses 108-20-3, Isopropyl ether 108-88-3, Toluene, uses 108-94-1, Cyclohexanone, uses 109-99-9, THF, uses 110-54-3, Hexane, uses 110-82-7, Cyclohexane, uses 110-86-1, Pyridine, uses 123-86-4, Butyl acetate 123-91-1, Dioxane, uses 141-78-6, Ethyl acetate, uses 142-82-5, Heptane, uses 563-80-4, Methyl isopropyl ketone 1330-20-7, Xylene, uses

RL: NUU (Other use, unclassified); USES (Uses)

(extg. **carotenoids**)

L7 ANSWER 8 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1995:489962 HCAPLUS

DOCUMENT NUMBER: 122:289068

TITLE: Bacteria belonging to new genus and process for production of **carotenoids** using same.

INVENTOR(S): Tsubokura, Akira; Yoneda, Hisashi; Takaki, Mikihiro; Kiyota, Takashi

PATENT ASSIGNEE(S): Nippon Oil Co., Ltd., Japan

SOURCE: Eur. Pat. Appl., 29 pp.

CODEN: EPXXDW

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|-----------------------|------|----------|-----------------|----------|
| EP 635576 | A1 | 19950125 | EP 1994-111525 | 19940722 |
| EP 635576 | B1 | 20000830 | | |
| R: CH, DE, FR, GB, LI | | | | |
| JP 07079796 | A2 | 19950328 | JP 1994-152240 | 19940704 |
| JP 3242531 | B2 | 20011225 | | |
| US 5607839 | A | 19970304 | US 1994-276943 | 19940719 |
| CA 2128549 | AA | 19950123 | CA 1994-2128549 | 19940721 |
| NO 9402731 | A | 19950123 | NO 1994-2731 | 19940721 |
| US 5858761 | A | 19990112 | US 1996-716841 | 19960919 |

PRIORITY APPLN. INFO.: JP 1993-181615 A 19930722

US 1994-276943 A3 19940719

AB Bacterium belonging to a new genus, and a process for prodn. of **carotenoid** pigment selected from the group consisting of astaxanthin, adonixanthin, .beta.-carotene, echinenone, canthaxanthin and zeaxanthin, comprising the steps of culturing a bacterium capable of producing at least one of the **carotenoid** pigments, and recovering an individual **carotenoid** pigments. The producer bacterium belongs to new genus. According to the present process various **carotenoids** can be produced in an industrial scale. By the present process (3S, 3'S)-astaxanthin can be produced in an almost 100% purity.

IT 472-61-7, (3S, 3'S)-Astaxanthin 4418-73-9, Adonixanthin

RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)

(bacteria belonging to new genus and process for prodn. of

MARX 09/049,228

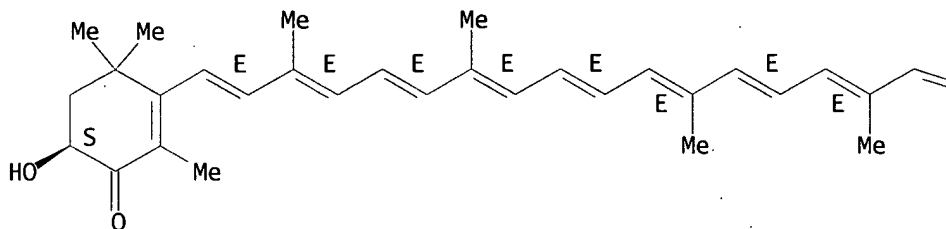
carotenoids using same)

RN 472-61-7 HCAPLUS

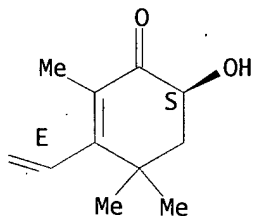
CN .beta.,.beta.-Carotene-4,4'-dione, 3,3'-dihydroxy-, (3S,3'S)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A



PAGE 1-B

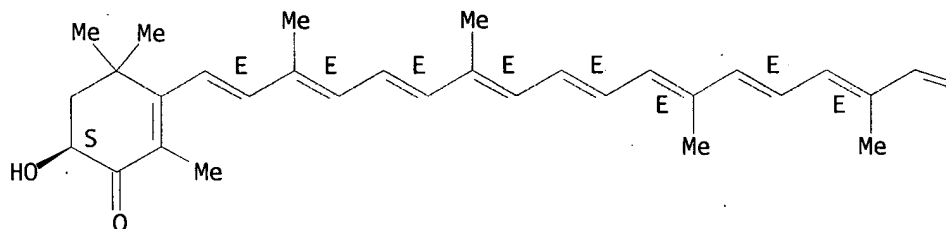


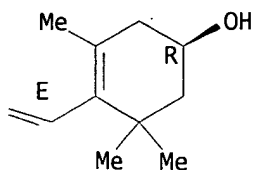
RN 4418-73-9 HCAPLUS

CN .beta.,.beta.-Caroten-4-one, 3,3'-dihydroxy-, (3S,3'R)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.
Double bond geometry as shown.

PAGE 1-A





IT 162875-45-8

RL: PRP (Properties)

(nucleotide sequence of; bacteria belonging to new genus and process for prodn. of **carotenoids** using same)

RN 162875-45-8 HCAPLUS

CN DNA (bacterium strain E-396 16S rRNA gene) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

IC ICM C12P025-00

ICS C12N001-20

CC 16-5 (Fermentation and Bioindustrial Chemistry)

ST **carotenoid** formation bacteria; astaxanthin formation bacteria; adonixanthin formation bacteria; rRNA 16S gene sequence bacteria

IT Bacteria

Deoxyribonucleic acid sequences

(bacteria belonging to new genus and process for prodn. of **carotenoids** using same)

IT Carotenes and **Carotenoids**, biological studies

RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)

(bacteria belonging to new genus and process for prodn. of **carotenoids** using same)

IT Gene, microbial

RL: PRP (Properties)

(bacteria belonging to new genus and process for prodn. of **carotenoids** using same)

IT Ribonucleic acids, ribosomal

RL: PRP (Properties)

(16 S, bacteria belonging to new genus and process for prodn. of **carotenoids** using same)

IT 472-61-7, (3S, 3'S)-Astaxanthin 4418-73-9, Adonixanthin

RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)

(bacteria belonging to new genus and process for prodn. of **carotenoids** using same)

IT 162875-45-8

RL: PRP (Properties)

(nucleotide sequence of; bacteria belonging to new genus and process for prodn. of **carotenoids** using same)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 09:18:53 ; Search time 5293 Seconds
(without alignments)
11222.516 Million cell updates/sec

Title: US-10-049-228-1

Perfect score: 1452

Sequence: 1 agtttgatccgtgctcagaa.....tgcgctggtacacatcctt 1452

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

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2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
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13: gb_un.*
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15: em_ba.*
16: em_fun.*
17: em_hum.*
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29: em_vt.*
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31: em_hgt_inv.*
32: em_hgt_other.*
33: em_hgt_mus.*
34: em_hgt_pln.*
35: em_hgt_rod.*
36: em_hgt_vrt.*
37: em_hgt_vrt.*
38: em_sy.*
39: em_hgt_hum.*
40: em_hgt_mus.*
41: em_hgt_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
|------------|--------|-------|--------|----|------------|--------------------|
| 1 | 1451 | 99.9 | 1452 | 1 | AB006899 | AB006899 Paracoccu |
| 2 | 1451 | 99.9 | 1452 | 6 | AR028747 | AR028747 Sequence |
| 3 | 1451 | 99.9 | 1452 | 6 | BD093842 | BD093842 A pigment |
| 4 | 1451 | 99.9 | 1452 | 6 | BD102673 | BD102673 A process |
| 5 | 1451 | 99.9 | 1452 | 6 | E14335 | E14335 DNA encodin |
| 6 | 1451 | 99.9 | 1452 | 6 | E40922 | E40922 Material co |
| 7 | 1451 | 99.9 | 1452 | 6 | I36531 | I36531 Sequence 1 |
| 8 | 1451 | 99.9 | 1452 | 6 | PM16SRNN | PM16SRNN Paracoccu |
| 9 | 1380 | 95.0 | 1426 | 6 | BD102674 | BD102674 A process |
| 10 | 1344.8 | 92.6 | 1360 | 1 | AB008114 | AB008114 Paracoccu |
| 11 | 1343.8 | 92.5 | 1408 | 1 | AB025190 | AB025190 Paracoccu |
| 12 | 1341.2 | 92.4 | 1456 | 1 | AY014177 | AY014177 Paracoccu |
| 13 | 1340.2 | 92.3 | 1450 | 1 | AY014169 | AY014169 Paracoccu |
| 14 | 1338.6 | 92.2 | 1461 | 1 | AY014170 | AY014170 Paracoccu |
| 15 | 1335.6 | 92.0 | 1453 | 1 | AY014168 | AY014168 Paracoccu |
| 16 | 1329.6 | 91.6 | 1420 | 1 | PAL294415 | AJ294415 Paracoccu |
| 17 | 1328.6 | 91.5 | 1409 | 1 | AB025192 | AB025192 Paracoccu |
| 18 | 1325.2 | 91.3 | 1416 | 1 | PSE428275 | AJ428275 Paracoccu |
| 19 | 1324.4 | 91.2 | 1458 | 1 | AY014176 | AY014176 Paracoccu |
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| 27 | 1297.8 | 89.4 | 1415 | 1 | AF461159 | AF461159 Paracoccu |
| 28 | 1296 | 89.3 | 1460 | 1 | AY014172 | AY014172 Paracoccu |
| 29 | 1294.8 | 89.2 | 1450 | 1 | AY014175 | AY014175 Paracoccu |
| 30 | 1293 | 89.0 | 1454 | 1 | PSP012068 | AJ012068 Paracoccu |
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| 33 | 1285.2 | 88.5 | 1349 | 1 | PSP391198 | AJ391198 Paracoccu |
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ALIGNMENTS

| RESULT 1 | AB006899 | AB006899 | 1452 bp | DNA | linear | BCT 10-MAR-1999 |
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| LOCUS | Paracoccus | carotinifaciens | gene for 16S rRNA, complete sequence. | | | |
| DEFINITION | AB006899 | | | | | |
| ACCESSION | AB006899 | | | | | |
| VERSION | AB006899.1 | GI:4514305 | | | | |
| KEYWORDS | 16S ribosomal RNA | | | | | |
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| ORGANISM | Paracoccus carotinifaciens | | | | | |
| REFERENCE | 1 (sites) | | | | | |
| AUTHORS | Tsubokura, A., Yoneda, H. and Mizuta, H. | | | | | |
| TITLE | Paracoccus carotinifaciens sp. nov., a new aerobic gram-negative astaxanthin-producing bacterium | | | | | |

Pred. No. is the number of results predicted by chance to have a

JOURNAL Int. J. Syst. Bacteriol. 49 Pt 1, 277-282 (1999)
MEDLINE 99152599
PUBMED 10028273
REFERENCE 2 (bases 1 to 1452)
AUTHORS Tsubokura, A.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-1997) Akira Tsubokura, Nippon Oil Company, Ltd.,
Central Technical Research Laboratory, 8, Chidori-cho, Naka-ku,
Yokohama, Kanagawa 231, Japan (E-mail: a-tsubokura@nissai.co.jp,
Tel: +81-45-625-7171, Fax: +81-45-625-7298)
FEATURES Location/Qualifiers
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DEFINITION Sequence 1 from patent US 5858761.
ACCESSION AR028747
VERSION AR028747.1 GI:5940720
KEYWORDS SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1452)
AUTHORS Tsubokura, A., Yoneda, H., Takaki, M. and Kiyota, T.
TITLE Bacteria for production of carotenoids
JOURNAL Patent: US 5858761-A 1 12-JAN-1999;
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RESULT 5
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LOCUS E14335 1452 bp DNA linear PAT 28-JUL-1999
DEFINITION DNA encoding 16S ribosome RNA of E-396 strain.
ACCESSION E14335
VERSION E14335.1 GI:5709018
KEYWORDS JP 1997308481-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1452)
AUTHORS Tsubokura, A., Yoneda, H., Uchiyama, Y. and Mizuta, Y.
TITLE COLOR TONE IMPROVER
JOURNAL Patent: JP 1997308481-A 1 02-DEC-1997;
NIPPON OIL CO LTD
COMMENT OS Unknown
PN JP 1997308481-A/1
PD 02-DEC-1997
PF 23-MAY-1996 JP 1996128565
PI TSUBOKURA AKIRA, YONEDA HISASHI, UCHIYAMA YOKO, PI MIZUTA YOSHINORI
PC C12N1/20, A23K1/16, A23K1/18, A23K1/18, A23L1/272, PC C09B1/00, C12N15/09,
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Matches 1452; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
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ACCESSION E40922
VERSION E40922.1 GI:2253150
KEYWORDS JP 2001095500-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1452)
AUTHORS Tsubokura,A., Yoneda,H. and Mizuta,Y.
TITLES Material containing dye for livestock addition
JOURNAL Patent: JP 2001095500-A 1 10-APR-2001;
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COMMENT OS Unknown
PN JP 2001095500-A/1
PD 30-SEP-1999 JP 1999279337
PI AKIRA Tsubokura, HISASHI YONEDA, YOSHITAKA MIZUTA PC
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BASE COUNT 353 a 346 c 461 g 291 t 1 others.

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1452; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTTGTCTCGGCTCAGAACGACGCTGGCGGAGGCTTAACATGCAAGTCAAGCGCA 60
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QY 1261 ATCCGGAACAGCATGCCGGGTGAATACGTTCCCGGGCTTGTACACACCGCCCGTCAAC 1320
Db 1261 ATCCGGAACAGCATGCCGGGTGAATACGTTCCCGGGCTTGTACACACCGCCCGTCAAC 1320
QY 1321 ACCATGGAGTGTGTTTACCCGACGACGNTGGCTTAACCTTCGGGGGGGAGGGGGCCAC 1380
Db 1321 ACCATGGAGTGTGTTTACCCGACGACGNTGGCTTAACCTTCGGGGGGGAGGGGGCCAC 1380
QY 1381 GGTAGGATCAGCAGTGGGTTGAAGTCTGAACAGGTAGCCGTAGGGGAGACCTCGCGCTG 1440

Db 1381 GGTAGGATCAGCAGTGGGTTGAAGTCTGAACAGGTAGCCGTAGGGGAACCTCGCGCTG 1440
QY 1441 GATCACCTCCTT 1452
Db 1441 GATCACCTCCTT 1452
RESULT 7
LOCUS I36531 1452 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 1 from patent US 5607839.
ACCESSION I36531
VERSION I36531.1 GI:2086356
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1452)
AUTHORS Tsubokura, A., Yoneda, H., Takaki, M. and Kiyota, T.
TITLE Bacteria belonging to new genus process for production of carotenoids using same
JOURNAL Patent: US 5607839-A 1 04-MAR-1997;
FEATURES
Location/Qualifiers
source 1. 1452
BASE COUNT 353 a 346 c 291 t 1 others
ORIGIN
Query Match 99.9%; Score 1451; DB 6; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1452; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGTTTGATCTCTGGCTCAGACGAAACGCTGGCGGAGGCTTAACACATGCAAGTCCGAGCGA 60
Db 1 AGTTTGATCTCTGGCTCAGACGAAACGCTGGCGGAGGCTTAACACATGCAAGTCCGAGCGA 60
QY 61 GACCTTCGGGTCTAGCGCGGACGCGGTGAGTAACGCTGGGAAACGCTTCTCTAGCG 120
Db 61 GACCTTCGGGTCTAGCGCGGACGCGGTGAGTAACGCTGGGAAACGCTTCTCTAGCG 120
QY 121 AATAGCCCCGGGAAACTGGGAGTAAATACCGTATACGCCCTTTGGGGGAAAGATTATCGG 180
Db 121 AATAGCCCCGGGAAACTGGGAGTAAATACCGTATACGCCCTTTGGGGGAAAGATTATCGG 180
QY 181 AGAAGGATCGGCCCGCTTGGATTAGGTAGTGGGTAAATGSCCCCAACCAAGCCGACG 240
Db 181 AGAAGGATCGGCCCGCTTGGATTAGGTAGTGGGTAAATGSCCCCAACCAAGCCGACG 240
QY 241 ATCCATAGCTGGTTTGAGAGGATGATCAGCCACACTGGGAGTGAACAGACGCGCCAGATC 300
Db 241 ATCCATAGCTGGTTTGAGAGGATGATCAGCCACACTGGGAGTGAACAGACGCGCCAGATC 300
QY 301 CTACGGAGGAGCAGCAGTGGGAAATCTTAGACAATGGGGCAACCCCTGATCTAGCCATGCC 360
Db 301 CTACGGAGGAGCAGCAGTGGGAAATCTTAGACAATGGGGCAACCCCTGATCTAGCCATGCC 360
QY 361 GCCTGAGTGATGAAGGCCTTAGGGTTGAAGCTCTTTTACGCTGGGAAGATAATAGCGGT 420
Db 361 GCCTGAGTGATGAAGGCCTTAGGGTTGAAGCTCTTTTACGCTGGGAAGATAATAGCGGT 420
QY 421 ACCAGCAGAGAGAGCCCGGCTTAACCTCGCTGCAGCAGCCGCGTATACGGAGGGGCT 480
Db 421 ACCAGCAGAGAGAGCCCGGCTTAACCTCGCTGCAGCAGCCGCGTATACGGAGGGGCT 480
QY 481 AGCGTTCTTCGGAAATCTAGGGCTAAAGCGCAGTAGGGGAGTCAAGAGTCAAGAGTG 540
Db 481 AGCGTTCTTCGGAAATCTAGGGCTAAAGCGCAGTAGGGGAGTCAAGAGTCAAGAGTG 540
QY 541 AATCCAGGGCTCAACCTTGGAACTGCCCTTTGAACATATCAGTCTGGAGTTCGAGAGAG 600
Db 541 AATCCAGGGCTCAACCTTGGAACTGCCCTTTGAACATATCAGTCTGGAGTTCGAGAGAG 600

| | | | | | | | |
|----|------|--------------|-------------------|----------------------|----------------------|--------------|------|
| Qy | 601 | GTGAGTGAATTC | CGAGTGTAGAGGTGA | AAATTCGTAGATATTC | CGAGGAACACCA | CGTGGC | 660 |
| Db | 601 | GTGAGTGAATTC | CGAGTGTAGAGGTGA | AAATTCGTAGATATTC | CGAGGAACACCA | CGTGGC | 660 |
| Qy | 661 | GAAGGGCGCT | CACTGGCTCGATAC | TACGCTGAGGTCC | GAAGCGTGGGAGCA | ACAGG | 720 |
| Db | 661 | GAAGGGCGCT | CACTGGCTCGATAC | TACGCTGAGGTCC | GAAGCGTGGGAGCA | ACAGG | 720 |
| Qy | 721 | ATTAGATAC | CCCTGGTAGTCC | ACGCCCTAAACGATGA | ATGCCAGACGTC | GCGAAGCATGCT | 780 |
| Db | 721 | ATTAGATAC | CCCTGGTAGTCC | ACGCCCTAAACGATGA | ATGCCAGACGTC | GCGAAGCATGCT | 780 |
| Qy | 781 | TGTCGGTGT | CACACCTTAACGGATTA | AGCATTCCTCGCCTGGGAGT | TACGTCGCAAGATTAA | 840 | |
| Db | 781 | TGTCGGTGT | CACACCTTAACGGATTA | AGCATTCCTCGCCTGGGAGT | TACGTCGCAAGATTAA | 840 | |
| Qy | 841 | AACTCAAAGAA | TTGACGGGGGCGGCAC | AAAGCGGTGGAGCATGT | GTTTAATCTCAAGC | 900 | |
| Db | 841 | AACTCAAAGAA | TTGACGGGGGCGGCAC | AAAGCGGTGGAGCATGT | GTTTAATCTCAAGC | 900 | |
| Qy | 901 | AACGGCAGAA | CCCTTACCAACCTTG | GATGGAGGACCGCT | CGAGAGATTACGTTTCT | 960 | |
| Db | 901 | AACGGCAGAA | CCCTTACCAACCTTG | GATGGAGGACCGCT | CGAGAGATTACGTTTCT | 960 | |
| Qy | 961 | CGTAAGAGAC | CTGCACACAGGTGCT | GATGGCTGCTGACGTC | GTGTGCGAGATGTTT | 1020 | |
| Db | 961 | CGTAAGAGAC | CTGCACACAGGTGCT | GATGGCTGCTGACGTC | GTGTGCGAGATGTTT | 1020 | |
| Qy | 1021 | GGTTAAGTC | CGGCAACGAGCGCA | ACCCACCTCCTAGTTGCC | AGCAATTCAGTTGGGAAC | 1080 | |
| Db | 1021 | GGTTAAGTC | CGGCAACGAGCGCA | ACCCACCTCCTAGTTGCC | AGCAATTCAGTTGGGAAC | 1080 | |
| Qy | 1081 | TCATGAAACT | GCCGATGATAGTC | CGGAGGAGGTGTG | GATCAGCTCAAGTCTCATGG | 1140 | |
| Db | 1081 | TCATGAAACT | GCCGATGATAGTC | CGGAGGAGGTGTG | GATCAGCTCAAGTCTCATGG | 1140 | |
| Qy | 1141 | GCCTTACGGGT | TGGGCTACACAGCTG | CTACAATGGTGGTG | GACAGTGGGTAAATCC | 1200 | |
| Db | 1141 | GCCTTACGGGT | TGGGCTACACAGCTG | CTACAATGGTGGTG | GACAGTGGGTAAATCC | 1200 | |
| Qy | 1201 | AGCCATCT | CAGTTCCGATCTG | CAACTCGAGGGCATGA | AGTTGGATCGCTAGTA | 1260 | |
| Db | 1201 | AGCCATCT | CAGTTCCGATCTG | CAACTCGAGGGCATGA | AGTTGGATCGCTAGTA | 1260 | |
| Qy | 1261 | ATCCGGAAC | AGCATGCGGGGTGA | ATACGTTCCCGGCCCTT | GACACCGGCCCTCAC | 1320 | |
| Db | 1261 | ATCCGGAAC | AGCATGCGGGGTGA | ATACGTTCCCGGCCCTT | GACACCGGCCCTCAC | 1320 | |
| Qy | 1321 | ACCATGGGAG | TTGGTTCTACCCGAC | GACGNTGGCTAAC | CTTCGGGGGGCAGCGGCCAC | 1380 | |
| Db | 1321 | ACCATGGGAG | TTGGTTCTACCCGAC | GACGNTGGCTAAC | CTTCGGGGGGCAGCGGCCAC | 1380 | |
| Qy | 1381 | GGTAGATC | AGCAGCTGGGGTGA | AGTCGTAAACAGGTAG | CCGTAGGGGAACCTT | CGCGCTG | 1440 |
| Db | 1381 | GGTAGATC | AGCAGCTGGGGTGA | AGTCGTAAACAGGTAG | CCGTAGGGGAACCTT | CGCGCTG | 1440 |
| Qy | 1441 | GATCAGCT | CTCCTT | 1452 | | | |
| Db | 1441 | GATCAGCT | CTCCTT | 1452 | | | |

RESULT 8

| | | | | | |
|------------|---|------------|-----|--------|-----------------|
| PM16SRRN | PM16SRRN | 1430 bp | DNA | linear | BCT 20-JUL-1998 |
| LOCUS | Paracoccus marcusii 16S rRNA gene. | | | | |
| DEFINITION | Y12703 | | | | |
| ACCESSION | Y12703.1 | GI:2765222 | | | |
| VERSION | 16S ribosomal RNA; 16S rRNA. | | | | |
| KEYWORDS | Paracoccus marcusii | | | | |
| SOURCE | Paracoccus marcusii | | | | |
| ORGANISM | Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Paracoccus. | | | | |
| REFERENCE | 1 | | | | |

| | | | |
|---|-----|---|-----|
| AUTHORS Harker, M., Hirschberg, J. and Oren, A. TITLE Paracoccus marcusii sp. nov., an orange gram-negative coccus JOURNAL Int. J. Syst. Bacteriol. 48 Pt 2, 543-548 (1998) MEDLINE 98401483 PUBMED 9731296 REFERENCE 2 (bases 1 to 1430) AUTHORS Hirschberg, J. TITLE Direct Submission JOURNAL Submitted (21-APR-1997) J. Hirschberg, The Hebrew University of Jerusalem, Dept of Genetics, Givat Ram, Jerusalem 91904, ISRAEL | | FEATURES Location/Qualifiers 1..1430 /organism="Paracoccus marcusii" /mol_type="genomic DNA" /db_xref="taxon:59779" { 1..1430 /gene="16S rRNA" <1..>1430 /gene="16S rRNA" /product="16S ribosomal RNA" 349 a 343 c 456 g 282 t | |
| BASE COUNT ORIGIN | | Query Match 97.48; Score 1414.8; DB 1; Length 1430; Best Local Similarity 99.7%; Pred. No. 0; Matches 142; Conservative 0; Mismatches 3; Indels 1; Gaps 1; | |
| Qy | 16 | CAGAACCAACGCTGGCGGCGAGGCTTAACACATGCAAGTCGAGCGAGACCTTCGGGTCTAG | 75 |
| Dd | 1 | CAGAACCAACGCTGGCGGCGAGGCTTAACACATGCAAGTCGAGCGAGACCTTCGGGTCTAG | 60 |
| Qy | 76 | CGCGGACGGGTGAGTAAACGCTGGGAAACGTCGCCCTTCTCTACGGAATACGCCCGGAAA | 135 |
| Dd | 61 | CGCGGACGGGTGAGTAAACGCTGGGAAACGTCGCCCTTCTCTACGGAATACGCCCGGAAA | 120 |
| Qy | 136 | CTGGGAGTATACCGTATAGCCCTTTGGGGGAAAGATTTATCGGAAAGATCGGCCCG | 195 |
| Dd | 121 | CTGGGAGTATACCGTATAGCCCTTTGGGGGAAAGATTTATCGGAAAGATCGGCCCG | 180 |
| Qy | 196 | CGTTGGATTAGTGTGGTGGGGTAATGGCCACCAAGCGACGATCCATAGCTGGTTT | 255 |
| Dd | 181 | CGTTGGATTAGTGTGGTGGGGTAATGGCCACCAAGCGACGATCCATAGCTGGTTT | 240 |
| Qy | 256 | GAGAGGATGATCAGCCACATGCGACTTGACACAGCGCCACAGCTCTACGGGAGGACGA | 315 |
| Dd | 241 | GAGAGGATGATCAGCCACATGCGACTTGACACAGCGCCACAGCTCTACGGGAGGACGA | 300 |
| Qy | 316 | GTGGGGAATCTAGACAATGGGCAACCCCTGATCTAGCCATGCCGGTGAGTGATGAAG | 375 |
| Dd | 301 | GTGGGGAATCTTAGACAATGGGGAACCCCTGATCTAGCCATGCCGGTGAGTGATGAAG | 360 |
| Qy | 376 | GCCTTAGGGTTGTAAGCTCTTCAGCTGGGAAGATAATACGGTACCCAGACAAGAAC | 435 |
| Dd | 361 | GCCTTAGGGTTGTAAGCTCTTCAGCTGGGAAGATAATACGGTACCCAGACAAGAAC | 420 |
| Qy | 436 | CCCGGCTAACTCCGTGCCACAGCCCGGTAATACGGAGGGGCTAGCGTTGTCGGAAT | 495 |
| Dd | 421 | CCCGGCTAACTCCGTGCCACAGCCCGGTAATACGGAGGGGCTAGCGTTGTCGGAAT | 480 |
| Qy | 496 | TACTGGCGGTAAAGCGCACGTAGCGGACGTGGAAGTACAGGTGAATCCGAGGGCTCA | 555 |
| Dd | 481 | TACTGGCGGTAAAGCGCACGTAGCGGACGTGGAAGTACAGGTGAATCCGAGGGCTCA | 540 |
| Qy | 556 | ACCTTTGAACTGCTTTTGAACATATCAGTCTGGAGTTCGAGAGAGGTGAGTGAATTCGG | 615 |
| Dd | 541 | ACCTTTGAACTGCTTTTGAACATATCAGTCTGGAGTTCGAGAGAGGTGAGTGAATTCGG | 600 |
| Qy | 616 | AGTGTAGAGGTGAATTCGTAGATATTCGGAGGAAACACCAAGTCGCGAGCGGCTCACTG | 675 |
| Dd | 601 | AGTGTAGAGGTGAATTCGTAGATATTCGGAGGAAACACCAAGTCGCGAGCGGCTCACTG | 660 |
| Qy | 676 | GCTCGATACGCTGAGTGGCGAAAGCGTGGGAGCAACACAGGATTAGTACCCTGGT | 735 |

| | | | |
|------|----|---|------|
| 661 | Db | GCTCGATCTGACGCTGAGGTTGCGGAAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGT | 720 |
| 736 | QY | AGTCCACGCGGTAATACGATGAATGCCAGACGTCGGCAAGCATGCTTGCGGTGTACACACC | 795 |
| 721 | Db | AGTCCACGCGGTAATACGATGAATGCCAGACGTCGGCAAGCATGCTTGCGGTGTACACACC | 780 |
| 796 | QY | TAAAGGATTAAAGCATTTCCGCTTGGGGAGTACGGTGCGAAGATTAAAACTCAAAGGAATTG | 855 |
| 781 | Db | TAAAGGATTAAAGCATTTCCGCTTGGGGAGTACGGTGCGAAGATTAAAACTCAAAGGAATTG | 840 |
| 896 | QY | ACGGGGGGCCGCACACAGCGGTGGAGCATGTGGTTTAAATTCGAAGCAACGCGCAGAACCTT | 915 |
| 841 | Db | ACGGGGGGCCGCACACAGCGGTGGAGCATGTGGTTTAAATTCGAAGCAACGCGCAGAACCTT | 900 |
| 916 | QY | ACCAACCCCTTGACATGGCAGACCGCTGGAGAGATTACGCTTCTCGTAAGACACCTGCA | 975 |
| 901 | Db | ACCAACCCCTTGACATGGCAGACCGCTGGAGAGATTACGCTTCTCGTAAGACACCTGCA | 960 |
| 976 | QY | CACAGGTGCTGCATGCTCTGCTGACCTCGTGCCTGCTGAGATGTTTCGTTAAAGTCCGGCAA | 1035 |
| 961 | Db | CACAGGTGCTGCATGCTCTGCTGACCTCGTGCCTGCTGAGATGTTTCGTTAAAGTCCGGCAA | 1020 |
| 1036 | QY | CGAGCGCAACCCACGCTCCCTAGTTGGCCAGAAATTCAGTTGGGAACTCTATGGAACACTGCC | 1095 |
| 1021 | Db | CGAGCGCAACCCACGCTCCCTAGTTGGCCAGC - ATTCAAGTTGGGCACCTCTATGGAACACTGCC | 1079 |
| 1096 | QY | GATTATAAGTCGGAGGAAGGTGGATGACGTCGAAGTCCCTCATGGGCCCTTACGGGTTGGG | 1155 |
| 1080 | Db | GATTATAAGTCGGAGGAAGGTGGATGACGTCGAAGTCCCTCATGGGCCCTTACGGGTTGGG | 1139 |
| 1156 | QY | CTACACACGCTGCTACAATGGTGGTGACAGTGGGTTAAATCCCAAAAAGCCATCTCAGTTCCG | 1215 |
| 1140 | Db | CTACACACGCTGCTACAATGGTGGTGACAGTGGGTTAAATCCCAAAAAGCCATCTCAGTTCCG | 1199 |
| 1216 | QY | GATTGTCTCTGCAACTCGAGGCGCATGAAGTTGGATTCGCTAGTAAATCGCGGAAACAGCAT | 1275 |
| 1200 | Db | GATTGTCTCTGCAACTCGAGGCGCATGAAGTTGGATTCGCTAGTAAATCGCGGAAACAGCAT | 1259 |
| 1276 | QY | GCCGCGGTGAATACGTTCCCGGGCCCTGTACACACCGCCGTCACACCAATGGGAGTTGGT | 1335 |
| 1260 | Db | GCCGCGGTGAATACGTTCCCGGGCCCTGTACACACCGCCGTCACACCAATGGGAGTTGGT | 1319 |
| 1336 | QY | TCTACCCGACGACGNTGCGCTAACCTTTCGGGGGGCAGCGGCCACCGTAGGATCAGCGCAC | 1395 |
| 1320 | Db | TCTACCCGACGACGCTGCGCTAACCTTTCGGGGGGCAGCGGCCACCGTAGGATCAGCGCAC | 1379 |
| 1396 | QY | TGGGGTGAAGTCTGATAAAGGTAGCCGTAGGGAAACCTCGCGCTGGATCAC | 1446 |
| 1380 | Db | TGGGGTGAAGTCTGATAAAGGTAGCCGTAGGGAAACCTCGCGCTGGATCAC | 1430 |

| | |
|------------|---|
| RESULT | 9. |
| BDI02674 | |
| LOCUS | 1426 bp DNA linear |
| DEFINITION | A process for producing carotenoid pigments. |
| ACCESSION | BDI02674 |
| VERSION | BDI02674.1 GI:22648248 |
| KEYWORDS | WO 0196591-A/2. |
| SOURCE | unidentified |
| ORGANISM | unclassified. |
| REFERENCE | 1. (bases 1 to 1426) |
| AUTHORS | Tsubokura, A. and Mizuta, H. |
| TITLE | A process for producing carotenoid pigments |
| JOURNAL | Patent: WO 0196591-A 2 20-DEC-2001; NIPPON MITSUBISHI OIL CORP, AKIRA TSUBOKURA, HARUYOSHI MIZUTA |
| COMMENT | OS Unknown PN WO 0196591-A/2 PD 20-DEC-2001 PF 08-JUN-2001 WO 2001JP004874 PR 12-JUN-2000 JP 00P I75124 PI AKIRA TSUBOKURA, HARUYOSHI MIZUTA PC C12P23/00 |

844 AACCTAAAGAAATTGACGGGGCCCGCACAGCGGTGGAGCATGTGTTAAATCGAGC 903
901 AACCGGAGAACCTTACCAACCTTGATGAGGAGGACCGCTGGAGAGATTCAGCTTTCT 960
904 AACCGGAGAACCTTACCAACCTTGATGAGGAGGACCGCTGGAGAGATTCAGCTTTCT 963
961 CGTAAGAGACCTGCACACAGGTGCTGATGGCTGCTGCTGAGCTGCTGCTGAGATGTC 1020
964 CGTAAGAGACCTGCACACAGGTGCTGATGGCTGCTGCTGAGCTGCTGCTGAGATGTC 1023
1021 GGTTAAGTCCGGCAACGAGGCGCAACCCACGCTCCCTAGTTGCCAGCAATTCAGTTGGGAAC 1080
1024 GGTTAAGTCCGGCAACGAGGCGCAACCCACGCTCCCTAGTTGCCAGC-ATTAGTTGGGCAC 1082
1081 TCATGGAACCTGCGGATGATAGTCGGAGGAGGTGATGATGATGATGATGATGATGATG 1140
1083 TCATGGAACCTGCGGATGATAGTCGGAGGAGGTGATGATGATGATGATGATGATGATG 1142
1141 GCCTTACGGGTGGGCTACACAGTGTCTACATGTTGTTGTTGTTGTTGTTGTTGTTGTT 1200
1143 CCCTTACGGGTGGGCTACACAGTGTCTACATGTTGTTGTTGTTGTTGTTGTTGTTGTT 1202
1201 AGCCATCTCAGTTCCGATTTGCTCTCAACTCGAGGCGATGAAGTTGGATGCTAGTA 1260
1203 AGCCATCTCAGTTCCGATTTGCTCTCAACTCGAGGCGATGAAGTTGGATGCTAGTA 1262
1261 ATCGCGAAGACGATGCGCGGTGAATACGTTCCCGGGCTTGTACACACCGCCGTCAC 1320
1263 ATCGCGAAGACGATGCGCGGTGAATACGTTCCCGGGCTTGTACACACCGCCGTCAC 1322
1321 ACCATGGAGTTGTTTCTACCGGACGAGTGGCTGAAC--TTCGGGGGGGAGCGGCC 1378
1323 ACCATGGAGTTGTTTCTACCGGACGAGTGGCTGAAC--TTCGGGGGGGAGCGGCC 1382
1379 ACGTAGGATCAGCGACTGGGGTGAAGTCTGTAACAGGTAGCC 1421
1383 ACGTAGGATCAGCGACTGGGGTGAAGTCTGTAACAGGTAGCC 1425

RESULT 10
AB008114
LOCUS AB008114 1360 bp DNA linear BCT 08-OCT-2002
DEFINITION Paracoccus sp. MBIC1143 gene for 16S rRNA, partial sequence.
ACCESSION AB008114
VERSION AB008114.1 GI:4512342
KEYWORDS
SOURCE Paracoccus sp. MBIC1143
ORGANISM Paracoccus sp. MBIC1143
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacteriales;
Rhodobacteraceae; Paracoccus.

REFERENCE 1
Misawa, N., Satomi, Y., Kondo, K., Yokoyama, A., Kajiura, S., Saito, T.,
Ohtani, T., and Miki, W.
Structure and functional analysis of a marine bacterial carotenoid
biosynthesis gene cluster and astaxanthin biosynthetic pathway
proposed at the gene level
J. Bacteriol. 177 (22), 6575-6584 (1995)
96062243
7592436

REFERENCE 2
Hamada, T., Yokoyama, A. and Harayama, S.
Paracoccus aurantiacus gen. nov., sp. nov., a new Carotenoid
Astaxanthin producing marine bacterium
Unpublished
3 (bases 1 to 1360)
Hamada, T.
Direct Submission
Submitted (14-OCT-1997) Tohru Hamada, Marine Biotechnology
Institute, Kamaishi Laboratories; 3-75-1 Heita, Kamaishi, Iwate
026-0001, Japan (E-mail: thamada@mano-enzyme.ne.jp,
Tel.: +81-193-26-6538, Fax: +81-193-26-6592)
Location/Qualifiers

FEATURES

1. 1360
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/db_xref="taxon:81397"
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/product="16S ribosomal RNA"
BASE COUNT 331 a 325 c 432 g 272 t
ORIGIN
Query Match 92.6%; Score 1344.8; DB 1; Length 1360;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1357; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 54 CGACGAGACCTTCGGGTCTAGCGCGGACGGGTGAGTAACCGTTCGGGAAAGTGCCTTC 113
DB 1 CGACGAGACCTTCGGGTCTAGCGCGGACGGGTGAGTAACCGTTCGGGAAAGTGCCTTC 60
QY 114 TCTACGGAATAGCCCCGGGAACTGGGAGTAATACCGTATACGCCCTTTGGGGAAAGAT 173
DB 61 TCTACGGAATAGCCCCGGGAACTGGGAGTAATACCGTATACGCCCTTTGGGGAAAGAT 120
QY 174 TTATCGGAGAGGATCGGCCCGCTTGGATTAGTAGTGTGGGGTAATGGCCCAACAA 233
DB 121 TTATCGGAGAGGATCGGCCCGCTTGGATTAGTAGTGTGGGGTAATGGCCCAACAA 180
QY 234 GCGACCATCATAGCTGTTTGGAGAGGATGATCAGCACACACTGGGACTGAGACACGGCC 293
DB 181 GCGACCATCATAGCTGTTTGGAGAGGATGATCAGCACACACTGGGACTGAGACACGGCC 240
QY 294 CAGACTCCTACGGGAGGACGAGTGGGAACTCTTAGACAATGGGGCAACCTGATCTAG 353
DB 241 CAGACTCCTACGGGAGGACGAGTGGGAACTCTTAGACAATGGGGCAACCTGATCTAG 300
QY 354 CCATGCCGCTGAGTATGATGAGGCTTAGGCTTGAAGCTCTTTCAGCTGGGAGATAA 413
DB 301 CCATGCCGCTGAGTATGATGAGGCTTAGGCTTGAAGCTCTTTCAGCTGGGAGATAA 360
QY 414 TGACGGTACGACGAGAGAGAGCCCGCTACTCCGTCAGCAGCGCGTAAATACGGA 473
DB 361 TGACGGTACGACGAGAGAGAGCCCGCTACTCCGTCAGCAGCGCGTAAATACGGA 420
QY 474 GGGGCTAGCGTGTTCGGGAATTAAGTGGCGTAAGGCGCAGCTAGGCGGACTGGAAGTC 533
DB 421 GGGGCTAGCGTGTTCGGGAATTAAGTGGCGTAAGGCGCAGCTAGGCGGACTGGAAGTC 480
QY 534 AGAGTGAATCCAGGGCTCAACCTTGGAACTGCCCTTTGAACTATCAGTCTGGAGTTC 593
DB 481 AGAGTGAATCCAGGGCTCAACCTTGGAACTGCCCTTTGAACTATCAGTCTGGAGTTC 540
QY 594 GAGAGGTCAGTGAATTCGGAGTGTAGAGTGAATTCGTAGATTCGAGAGAACAC 653
DB 541 GAGAGGTCAGTGAATTCGGAGTGTAGAGTGAATTCGTAGATTCGAGAGAACAC 600
QY 654 CAGTGGCGAAGGGGCTCACTGGCTCGATACGCTGAGGTGAGGTGCGAAGCGTGGGGAGC 713
DB 601 CAGTGGCGAAGGGGCTCACTGGCTCGATACGCTGAGGTGCGAAGCGTGGGGAGC 660
QY 714 AACAGGATAGATACCTCGTGTAGTCCACCGCTTAAACGATGAATGCCAGACGTCGGCAA 773
DB 661 AACAGGATAGATACCTCGTGTAGTCCACCGCTTAAACGATGAATGCCAGACGTCGGCAA 720
QY 774 GCATGCTTGTGGTGTACACCTAACCGATTAACGATTAACGATTAACGATTAACGATTA 833
DB 721 GCATGCTTGTGGTGTACACCTAACCGATTAACGATTAACGATTAACGATTAACGATTA 780
QY 834 AGATAAAGCTCAAGGAAATGACGGGGCGCCGACAAAGCGGTGGAGCATGTGTTTAAAT 893
DB 781 AGATAAAGCTCAAGGAAATGACGGGGCGCCGACAAAGCGGTGGAGCATGTGTTTAAAT 840

| Db | 1021 | CAACCCACGTCCTAGTTGCCAGC -ATTCAAGTTGGGCACTCTATGGAAATCGCCGATGAT | 1079 |
|-----------------------|------|---|------|
| Qy | 1102 | AAGTCGGAGGAAGTGTGGATGACGTCAAGTCTCTCATGGCCCTTACGGGTGGGCTACAC | 1161 |
| Db | 1080 | AAGTCGGAGGAAGTGTGGATGACGTCAAGTCTCTCATGGCCCTTACGGGTGGGCTACAC | 1139 |
| Qy | 1162 | ACGTGCTACAAATGGTGTGACGTGAGTGGGTTAATCCCAAAAGCCATCTCAGTTTCGGATTGT | 1221 |
| Db | 1140 | ACGTGCTACAAATGGTGTGACGTGAGTGGGTTAATCCCAAAAGCCATCTCAGTTTCGGATTGT | 1199 |
| Qy | 1222 | CCCTGCAACTCGAGGGCATGAAGTTGGAAATCGCTAGTAAATCGCGGAACAGCATGCCGGG | 1281 |
| Db | 1200 | CCCTGCAACTCGAGGGCATGAAGTTGGAAATCGCTAGTAAATCGCGGAACAGCATGCCGGG | 1259 |
| Qy | 1282 | GTGAATACGTTCCGGGCTTGTACACACCGCCGCTACACCATGGAGTTGGTTCTACC | 1341 |
| Db | 1260 | GTGAATACGTTCCGGGCTTGTACACACCGCCGCTACACCATGGAGTTGGTTCTACC | 1319 |
| Qy | 1342 | CGACGACGNTGCGCTTAACCTTCGGGGGGGAGCGGCGCACGGTAGGATCAGCGACTGGGT | 1401 |
| Db | 1320 | CGACGACGNTGCGCTTAACCTTCGGGGGGGAGCGGCGCACGGTAGGATCAGCGACTGGGT | 1379 |
| Qy | 1402 | GAAGTCCTAACAGGTAGCGTAGGGGA | 1429 |
| Db | 1380 | GAAGTCCTAACAGGTAGCGTAGGGGA | 1407 |
| RESULT 12 | | | |
| AV014177 | | 1456 bp DNA linear BCT 10-MAR-2003 | |
| LOCUS | | Paracoccus alcaliphilus 16S ribosomal RNA gene, partial sequence. | |
| DEFINITION | | Paracoccus alcaliphilus | |
| ACCESSION | | AV014177 | |
| KEYWORDS | | AV014177.1 GI:13489271 | |
| SOURCE | | Paracoccus alcaliphilus | |
| ORGANISM | | Paracoccus alcaliphilus | |
| REFERENCE | | Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales; | |
| AUTHORS | | 1 (bases 1 to 1456) | |
| | | Daneshvar,M.I., Hollis,D.G., Weyant,R.S., Steigerwalt,A.G., | |
| | | Whitney,A.M., Douglas,M.P., Macgregor,J.P., Jordan,J.G., | |
| | | Mayer,L.W., Rassouli,S.M., Marchet,W., Munro,C., Shuttleworth,L. | |
| | | and Bernard,K. | |
| TITLE | | Paracoccus yeell sp. nov. (Formerly CDC Group EO-2), a Novel | |
| JOURNAL | | Bacterial Species Associated with Human Infection | |
| PUBMED | | 12624070 | |
| REFERENCE | | 2 (bases 1 to 1456) | |
| AUTHORS | | Douglas,M.P., Weyant,R.S., Hollis,D.G., Jordan,J., Macgregor,J., | |
| | | Steigerwalt,A.G. and Daneshvar,M.I. | |
| TITLE | | Direct Submission | |
| JOURNAL | | Submitted (16-NOV-2000) NCID/DBMD/MSPB/SBRL, Centers for Disease | |
| FEATURES | | Control and Prevention, 1600 Clifton Road, Atlanta, GA 30333, USA | |
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VERSION AY014169.1 GI:13489263
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ORGANISM Paracoccus yeii
REFERENCE 1 (bases 1 to 1460)
AUTHORS Daneshvar M.I., Hollis D.G., Weyant R.S., Steigerwalt A.G.,
Whitney A.M., Douglas M.P., Macgregor J.P., Jordan J.G.,
Mayer L.W., Rassouli S.M., Barchet W., Munro C., Shuttleworth L.
and Bernard K.
TITLE Paracoccus yeii sp. nov. (Formerly CDC Group EO-2), a Novel
Bacterial Species Associated with Human Infection
JOURNAL J. Clin. Microbiol. 41 (3), 1289-1294 (2003)
PUBMED 12624070
AUTHORS Douglas M.P., Weyant R.S., Hollis D.G., Jordan J., Macgregor J.,
Steigerwalt A.G. and Daneshvar M.I.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2000) NCID/DBMD/MSBP/SBRL, Centers for Disease
Control and Prevention, 1600 Clifton Road, Atlanta, GA 30333, USA
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REFERENCE 1 (bases 1 to 1461)
AUTHORS Daneshvar,M.I., Hollis,D.G., Weyant,R.S., Steigewalt,A.G.,
Whitney,A.M., Douglas,M.P., Macgregor,J.P., Jordan,J.G.,
Mayer,L.W., Rassouli,S.M., Barchet,W., Munro,C., Shuttleworth,L.
and Bernard,K.
TITLE Paracoccus yeeli sp. nov. (Formerly CDC Group EO-2), a Novel
Bacterial Species Associated With Human Infection
JOURNAL J. Clin. Microbiol. 41 (3), 1289-1294 (2003)
PUBMED 15624070
REFERENCE 2 (bases 1 to 1461)
AUTHORS Douglas,M.P., Weyant,R.S., Hollis,D.G., Jordan,J., Macgregor,J.,
Steigewalt,A.G. and Daneshvar,M.I.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2000) NCID/DBMD/MSPE/SBRL, Centers for Disease
Control and Prevention, 1600 Clifton Road, Atlanta, GA 30333, USA
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AUTHORS Daneshvar,M.I., Hollis,D.G., Weyant,R.S., Steigerwalt,A.G.,
Whitney,A.M., Douglas,M.P., Macgregor,J.P., Jordan,J.G.,
Mayer,L.W., Rassouli,S.M., Barchet,W., Munro,C., Shuttleworth,L.
and Bernard,K.
TITLE Paracoccus yeeli sp. nov. (Formerly CDC Group EO-2), a Novel
Bacterial Species Associated with Human Infection
JOURNAL J. Clin. Microbiol. 41 (3), 1285-1294 (2003)
PUBMED 12624070
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AUTHORS Douglas,M.P., Weyant,R.S., Hollis,D.G., Jordan,J., Macgregor,J.,
Steigerwalt,A.G. and Daneshvar,M.I.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2000) NCID/DBMD/MSBP/SBRU, Centers for Disease
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Copyright (c) 1993 - 2003 CompuGen Ltd.

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- 11: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
- 12: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
- 13: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
- 14: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
- 15: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
- 16: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
- 17: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
- 18: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
- 19: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
- 20: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
- 21: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
- 22: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
- 23: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
- 24: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
- 25: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1451 | 99.9 | 1452 | 17 | AA115842 |
| 2 | 1451 | 98.9 | 1452 | 19 | AAV22896 |
| 3 | 1451 | 99.9 | 1452 | 22 | AAV82204 |
| 4 | 1451 | 99.9 | 1452 | 24 | ABL40151 |
| 5 | 1439 | 99.1 | 1451 | 16 | AAQ81791 |
| 6 | 1414.8 | 97.4 | 1430 | 20 | AAQ07384 |
| 7 | 1380 | 95.0 | 1426 | 24 | ABL40152 |
| 8 | 1246.2 | 85.8 | 1452 | 24 | ABL55950 |

DNA derived from 1
DNA encoding a col
DNA sequence used
16S ribosomal RNA
Nucleotide sequenc
Paracoccus marcusii
16S ribosomal RNA
Rhodobacter sphaer

| | | | | | |
|----|--------|------|------|----|----------|
| 9 | 1246.2 | 85.8 | 1462 | 24 | ABL55996 |
| 10 | 1244.4 | 85.7 | 1426 | 20 | AAV03559 |
| 11 | 1227.2 | 84.5 | 1407 | 22 | AAH48039 |
| 12 | 1205.4 | 83.0 | 1430 | 22 | AAV87598 |
| 13 | 1205.4 | 83.0 | 1430 | 22 | AAH40356 |
| 14 | 1113.2 | 76.7 | 1484 | 24 | ABL55947 |
| 15 | 1113.2 | 75.7 | 1484 | 24 | ABL55993 |
| 16 | 1098.6 | 75.7 | 1405 | 22 | AAH49546 |
| 17 | 1093.6 | 75.3 | 1466 | 22 | AAH41032 |
| 18 | 1086.4 | 74.8 | 1502 | 20 | AAV72293 |
| 19 | 1082.6 | 74.6 | 1450 | 22 | AAV90275 |
| 20 | 1044.6 | 71.9 | 1490 | 24 | ABL54570 |
| 21 | 1024.4 | 70.6 | 1446 | 17 | AAV10955 |
| 22 | 1002.4 | 69.0 | 1446 | 25 | ABZ26100 |
| 23 | 987.4 | 68.0 | 1450 | 20 | AAH82005 |
| 24 | 973.6 | 67.1 | 1436 | 21 | AAZ45683 |
| 25 | 969.8 | 66.8 | 1479 | 24 | ABV71617 |
| 26 | 969.2 | 66.7 | 1321 | 24 | ABL55948 |
| 27 | 967.6 | 66.6 | 1319 | 24 | ABL55994 |
| 28 | 967.6 | 66.6 | 1319 | 24 | ABL55995 |
| 29 | 967.6 | 66.6 | 1319 | 24 | ABL55995 |
| 30 | 967.6 | 66.6 | 1319 | 24 | ABL55995 |
| 31 | 960.4 | 66.1 | 1438 | 21 | AAZ45682 |
| 32 | 947.6 | 65.3 | 1500 | 22 | AAV89988 |
| 33 | 939.4 | 64.7 | 1360 | 22 | AAV89982 |
| 34 | 939.2 | 64.7 | 1225 | 22 | AAV89990 |
| 35 | 937.2 | 64.5 | 1500 | 22 | AAV89980 |
| 36 | 936 | 64.5 | 1361 | 22 | AAV90021 |
| 37 | 929 | 64.0 | 1223 | 22 | AAV89985 |
| 38 | 928.4 | 63.9 | 1535 | 20 | AAV83569 |
| 39 | 920.2 | 63.4 | 1237 | 22 | AAV89986 |
| 40 | 918.8 | 63.3 | 1535 | 20 | AAV83568 |
| 41 | 916.4 | 63.1 | 1528 | 20 | AAV83570 |
| 42 | 906 | 62.4 | 1346 | 22 | AAV89987 |
| 43 | 904.8 | 62.3 | 1208 | 20 | AAV72292 |
| 44 | 900.6 | 62.0 | 1288 | 22 | AAV89983 |
| 45 | 900.6 | 62.0 | 1529 | 20 | AAV83564 |

ALIGNMENTS

RESULT 1
AA115842
ID AA115842 standard; DNA; 1452 BP.
XX
AC AA115842;
XX
DF 15-AUG-1996 (first entry)
XX
DE DNA derived from 16S ribosomal RNA.
XX
KW 16S rRNA; E-396 (FERM BP-4283); A-581-1 (FERM BP-4671);
KW all-trans astaxanthin; ss;
XX
OS E-396 (FERM BP-4283).
XX
PN JP08009964-A.
XX
PD 16-JAN-1996.
XX
PF 04-JUL-1994; 94JP-0152078.
XX
PR 04-JUL-1994; 94JP-0152078.
XX
PA (NIOC) NIPPON OIL CO LTD.
XX
DR WPI; 1996-110265/12.
XX
PT New microbes E-396 and A-581-1 - useful for prodn. of all-trans
XX astaxanthin
XX
PS Disclosure; Page 17-18; 20pp; Japanese.

xx This sequence represents the 16S rRNA gene from a new species of
cc microbe, E-396 (FERM BP-4283). The microbe is a gram negative
cc pleomorphic rod shaped motile microbe which is aerobic. The GC
cc content of the intracellular DNA is 64-69%. The microbe may be used
cc in the production of all-trans astaxanthin in high yield.
xx
xx
sq Sequence 1452 BP; 353 A; 346 C; 461 G; 291 T; 1 other;

CC from a culture of the microorganisms designated E-396 (FERM BP-4283)
 CC or its mutant A-581-1 (FERM BP-4671). When the protein was fed to white
 CC leghorn chickens, the colour of their egg yolks improved. The colour
 CC improver improves the colour of foods and drinks.

XX Sequence 1452 BP; 353 A; 346 C; 461 G; 291 T; 1 other;

Query Match 99.9%; Score 1451; DB 19; Length 1452;
 Best Local Similarity 100.08; Pred. No. 0;
 Matches 1452; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTTGTGCTCGGCTCAGAACGAGCTGGGGGAGGCTTAACACATCAAGTCGAGGGA 60
 DB 1 AGTTTGTGCTCGGCTCAGAACGAGCTGGGGGAGGCTTAACACATCAAGTCGAGGGA 60

QY 61 GACCTTCGGGCTAGCGGCGGACGGGTGAGTAACCGCTGGGGAACCTGCTCTACGG 120
 DB 61 GACCTTCGGGCTAGCGGCGGACGGGTGAGTAACCGCTGGGGAACCTGCTCTACGG 120

QY 121 AATAGCCCGGAACTGGGAGTAATACGATATACGCTTGGGGGAAAGATTATCGG 180
 DB 121 AATAGCCCGGAACTGGGAGTAATACGATATACGCTTGGGGGAAAGATTATCGG 180

QY 181 AGAAGGATCGGCCCGCTTGGATTAGTGTGGGTATGGCCCAACCAAGCCGAGC 240
 DB 181 AGAAGGATCGGCCCGCTTGGATTAGTGTGGGTATGGCCCAACCAAGCCGAGC 240

QY 241 ATCCATAGCTGGTTGAGAGATGATCAGCCACACTGGGACTGAGACAGGCCCAAGACTC 300
 DB 241 ATCCATAGCTGGTTGAGAGATGATCAGCCACACTGGGACTGAGACAGGCCCAAGACTC 300

QY 301 CTACGGGAGGACGAGTGGGAACTTAGACATAGGGGCAACCTGTAGTACCATGCC 360
 DB 301 CTACGGGAGGACGAGTGGGAACTTAGACATAGGGGCAACCTGTAGTACCATGCC 360

QY 361 CGGTGAGTGAAGGCTTAGGGTTGTAAGACTCTTTCAGCTGGGGAAGATAATGACGCT 420
 DB 361 CGGTGAGTGAAGGCTTAGGGTTGTAAGACTCTTTCAGCTGGGGAAGATAATGACGCT 420

QY 421 ACCAGCAGAAGACCCCGGCTAATCCGTGCGCAGCCGCGGTAAATACGAGGGGCT 480
 DB 421 ACCAGCAGAAGACCCCGGCTAATCCGTGCGCAGCCGCGGTAAATACGAGGGGCT 480

QY 481 AGCGTGTGCGGAATTAAGGCGTAAAGCGCACCTAGGCGACTGGAAGTCAGAGTG 540
 DB 481 AGCGTGTGCGGAATTAAGGCGTAAAGCGCACCTAGGCGACTGGAAGTCAGAGTG 540

QY 541 AAATCCAGGGCTCAACCTTGGAACTGCTTGAACATATCAGTCTGGAGTTCGAGAGAG 600
 DB 541 AAATCCAGGGCTCAACCTTGGAACTGCTTGAACATATCAGTCTGGAGTTCGAGAGAG 600

QY 601 GTGAGTGAATTCGAGTGTAGAGTGAAATTCGTAGATATTCGGAGGAACACCAAGTGGC 660
 DB 601 GTGAGTGAATTCGAGTGTAGAGTGAAATTCGTAGATATTCGGAGGAACACCAAGTGGC 660

QY 661 GAAGCGGCTCACTGGCTGATCTAGCTGAGTGGGAAAGCGTGGGGACCAACAGG 720
 DB 661 GAAGCGGCTCACTGGCTGATCTAGCTGAGTGGGAAAGCGTGGGGACCAACAGG 720

QY 721 ATTAGATACCTGGTGTAGTCCCGCTTAAAGCATGAATGCCAGAGCTGGCAAGCATGCT 780
 DB 721 ATTAGATACCTGGTGTAGTCCCGCTTAAAGCATGAATGCCAGAGCTGGCAAGCATGCT 780

QY 781 TGTGCGGTCTACACCTAAGGATTAAGCATTCGCGCTGGGAGTACGGTTCGCAAGATTAA 840
 DB 781 TGTGCGGTCTACACCTAAGGATTAAGCATTCGCGCTGGGAGTACGGTTCGCAAGATTAA 840

QY 841 AACTCAAGGAATTGACGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAAATCGAAGC 900
 DB 841 AACTCAAGGAATTGACGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAAATCGAAGC 900

QY 901 AACGGCGAGACCTTACCAACCTTGACATGGCAGGACCGCTGGAGAGATTCAGCTTCT 960
 DB 901 AACGGCGAGACCTTACCAACCTTGACATGGCAGGACCGCTGGAGAGATTCAGCTTCT 960

DB 901 AACGGCGAGACCTTACCAACCTTGACATGGCAGGACCGCTGGAGAGATTCAGCTTCT 960
 QY 961 CGTAGAGACCTGCGACACAGAGTGTGTCATGGCTGTGTCAGCTGTGTCGTGAGATGTC 1020
 DB 961 CGTAGAGACCTGCGACACAGAGTGTGTCATGGCTGTGTCAGCTGTGTCGTGAGATGTC 1020

QY 1021 GGTTAAGTCCGGCAACGAGCGCAACCCAGTCCCTAGTTGCCAGCAATTCAGTTGGGAAC 1080
 DB 1021 GGTTAAGTCCGGCAACGAGCGCAACCCAGTCCCTAGTTGCCAGCAATTCAGTTGGGAAC 1080

QY 1081 TCTATGGAACCTGCCGATGATAAGTCGGAGGAAGGTGTGATGACGTCAAGTCTCATGG 1140
 DB 1081 TCTATGGAACCTGCCGATGATAAGTCGGAGGAAGGTGTGATGACGTCAAGTCTCATGG 1140

QY 1141 GCCTTACGGTTGGGCTACACACGCTGCTACAATGGTGTGACAGTGGTTAATCCCAAA 1200
 DB 1141 GCCTTACGGTTGGGCTACACACGCTGCTACAATGGTGTGACAGTGGTTAATCCCAAA 1200

QY 1201 AGCCATCTCAGTTCGGATTGTCTCTGCAACTCGAGGGCATGAAGTTGGAATCGCTAGTA 1260
 DB 1201 AGCCATCTCAGTTCGGATTGTCTCTGCAACTCGAGGGCATGAAGTTGGAATCGCTAGTA 1260

QY 1261 ATFCGCGGAACAGCATGCGCGGTGAATACGTTCCCGGGCTTGTACACACCCCGCTCAC 1320
 DB 1261 ATFCGCGGAACAGCATGCGCGGTGAATACGTTCCCGGGCTTGTACACACCCCGCTCAC 1320

QY 1321 ACCATGGGAGTTGGTTCTACCCGACGACGNTCGGCTAACCTTCGGGGGCGACGGCCAC 1380
 DB 1321 ACCATGGGAGTTGGTTCTACCCGACGACGNTCGGCTAACCTTCGGGGGCGACGGCCAC 1380

QY 1381 GGTAGGATCAGGACTGGGGTGAAGTCGTAACAAGTAGCCGTAGGGGAACCTGCGGGCTG 1440
 DB 1381 GGTAGGATCAGGACTGGGGTGAAGTCGTAACAAGTAGCCGTAGGGGAACCTGCGGGCTG 1440

QY 1441 GATCACCTCCTT 1452
 DB 1441 GATCACCTCCTT 1452

RESULT 3

AAF82204

ID AAF82204 standard; DNA; 1452 BP.

XX AAF82204;

XX AAF82204;

DT 05-JUN-2001 (first entry)

XX DNA sequence used in the production of pigment-containing feed additive.
 XX Animal feed; foodstuff; pigment-containing; feed additive; ds.

XX Unidentified.

XX WO200122833-A1.

XX 05-APR-2001.

XX 22-SEP-2000; 2000WO-JP06528.

XX 30-SEP-1999; 99JP-0279337.

XX (MISQ) NIPPON MITSUBISHI OIL CORP.

XX Tsukubura A, Yoneda H, Mizuta H;

XX WPI; 2001-258066/26.

XX Microbial culture precipitate with high carotenoid content for

XX production of high stability animal foodstuffs -

XX Claim 3; Page 12-13; 18pp; Japanese.

XX The present sequence is provided in a specification relating to a

XX

PS Claim 2; Page 17-18; 23pp; Japanese.

XX The present invention describes a microbial method for producing
CC carotenoid compounds at a specified, or varying, ratio by controlling
CC the concentration of oxygen dissolved in the liquid medium during
CC culture. The produced carotenoids are natural pigments, which are useful
CC in feed additives, food additives and pharmaceuticals. The ratio of the
CC carotenoid compounds obtained can be controlled by varying the
CC concentration of oxygen dissolved in liquid medium during culture.
CC The present sequence represents a specifically claimed 16S ribosomal RNA
CC gene from an unknown organism designated E-396, from the present
CC invention.

SQ Sequence 1452 BP; 353 A; 346 C; 461 G; 291 T; 1 other;

| | | | | | |
|-----------------------|-----|--|---------------|-----------|--------------|
| Query Match | | 99.9%; | Score 1451; | DB 24; | Length 1452; |
| Best Local Similarity | | 100.0%; | Pred. No. 0; | | |
| Matches 1452; | | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| QY | 1 | AGTTTGATCTGGCTCAGACGAACGCTGGCGGAGGCTTACACATCAAGTCGAGCGA | 60 | | |
| DB | 1 | AGTTTGATCTGGCTCAGACGAACGCTGGCGGAGGCTTACACATCAAGTCGAGCGA | 60 | | |
| QY | 61 | GACCTTCGGGTCTAGCGCGGACGCGGTGAGTAACGCTGGGAACGTCCTTCTCTACGG | 120 | | |
| DB | 61 | GACCTTCGGGTCTAGCGCGGACGCGGTGAGTAACGCTGGGAACGTCCTTCTCTACGG | 120 | | |
| QY | 121 | AATAGCCCCGGAACTGGGAGTAAATACCGTATACGCCCTTTGGGGAAAGATTATCGG | 180 | | |
| DB | 121 | AATAGCCCCGGAACTGGGAGTAAATACCGTATACGCCCTTTGGGGAAAGATTATCGG | 180 | | |
| QY | 181 | AGAGGATCGCCCGCTTGATAGTAGTGTGGGGTAAATGGCCCAACGACCGACG | 240 | | |
| DB | 181 | AGAGGATCGCCCGCTTGATAGTAGTGTGGGGTAAATGGCCCAACGACCGACG | 240 | | |
| QY | 241 | ATCATAGCTGTTTGAGAGGATGATCAGCCACACCTGGGACTGGAGACGCGCCAGACTC | 300 | | |
| DB | 241 | ATCATAGCTGTTTGAGAGGATGATCAGCCACACCTGGGACTGGAGACGCGCCAGACTC | 300 | | |
| QY | 301 | CTACGGAGGAGCAGTGGGGAATCTTAGACAAATGGGGCAACCTGATCTAGCCATGCC | 360 | | |
| DB | 301 | CTACGGAGGAGCAGTGGGGAATCTTAGACAAATGGGGCAACCTGATCTAGCCATGCC | 360 | | |
| QY | 361 | CGGTGAGTGATGAAGCCCTTAGGTTGTAAGCTCTTTCAGCTGGGAAGATAATGACGGT | 420 | | |
| DB | 361 | CGGTGAGTGATGAAGCCCTTAGGTTGTAAGCTCTTTCAGCTGGGAAGATAATGACGGT | 420 | | |
| QY | 421 | ACCAGCAGAAGAACCCCGGCTAACTCGTCCAGCAGCGCGGTAATACGGAGGGGCT | 480 | | |
| DB | 421 | ACCAGCAGAAGAACCCCGGCTAACTCGTCCAGCAGCGCGGTAATACGGAGGGGCT | 480 | | |
| QY | 481 | AGCGTGTTCGGAATTAAGTGGCGTAAGACGACGCTAGCGGACTGGAAAGTCAGAGTG | 540 | | |
| DB | 481 | AGCGTGTTCGGAATTAAGTGGCGTAAGACGACGCTAGCGGACTGGAAAGTCAGAGTG | 540 | | |
| QY | 541 | AAATCCAGGAGGCTCAACCTTGGACTGCTTTGAACTATCAGTCTGGAGTTCGAGAG | 600 | | |
| DB | 541 | AAATCCAGGAGGCTCAACCTTGGACTGCTTTGAACTATCAGTCTGGAGTTCGAGAG | 600 | | |
| QY | 601 | GTGAGTGGAAATCCGAGTGTAGAGTGAATTCGTAGATATTCGGAGGAACACCAAGTGGC | 660 | | |
| DB | 601 | GTGAGTGGAAATCCGAGTGTAGAGTGAATTCGTAGATATTCGGAGGAACACCAAGTGGC | 660 | | |
| QY | 661 | GAAGCGGCTCACTGGCTGATCTAGCTGAGGTGGAAAGGCTGGGGAGCAACACAGG | 720 | | |
| DB | 661 | GAAGCGGCTCACTGGCTGATCTAGCTGAGGTGGAAAGGCTGGGGAGCAACACAGG | 720 | | |
| QY | 721 | ATTAGATACCTGTGTAGTCCACGCGGTAAACGATGAATGCGAGAGTTCGGCAAGCATGCT | 780 | | |
| DB | 721 | ATTAGATACCTGTGTAGTCCACGCGGTAAACGATGAATGCGAGAGTTCGGCAAGCATGCT | 780 | | |
| QY | 781 | TGTCGGTGTACACCTACGATTAAGCATTTCCGCTGGGAGTACGGTCGCAAGATTAA | 840 | | |

| | | | |
|----|------|--|------|
| DB | 781 | TGTCGGTGTACACCTACGGATTAAAGCATTCGCGCTGGGAGTAGCGTCAAGATTAA | 840 |
| QY | 841 | AACTCAAGAGTAATGACGGGGCCGCGCACAAAGCGTGGAGCATGTGGTTAATTCGAAGC | 900 |
| DB | 841 | AACTCAAGAGTAATGACGGGGCCGCGCACAAAGCGTGGAGCATGTGGTTAATTCGAAGC | 900 |
| QY | 901 | AACGGCGAGACCTTACCAACCTTTGACATGCGAGGACCGCTGGAGAGTTCAGCTTCT | 960 |
| DB | 901 | AACGGCGAGACCTTACCAACCTTTGACATGCGAGGACCGCTGGAGAGTTCAGCTTCT | 960 |
| QY | 961 | CGTAAGAGACCTGCGACAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 1020 |
| DB | 961 | CGTAAGAGACCTGCGACAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 1020 |
| QY | 1021 | GTTAAGTCCGCAACAGAGCGCAACCCAGTCCCTAGTTGCGAGCAATTCAGTTGGGAAC | 1080 |
| DB | 1021 | GTTAAGTCCGCAACAGAGCGCAACCCAGTCCCTAGTTGCGAGCAATTCAGTTGGGAAC | 1080 |
| QY | 1081 | TCTATGGAACCTGCGATGATTAAGTCGGAGGAGGTGCGATGAGTCAAGTCCCTCATGG | 1140 |
| DB | 1081 | TCTATGGAACCTGCGATGATTAAGTCGGAGGAGGTGCGATGAGTCAAGTCCCTCATGG | 1140 |
| QY | 1141 | GCCTTACCGGTTGGCTTACACACGCTGCTACAATGCTGAGTGGGTAAATCCCAA | 1200 |
| DB | 1141 | GCCTTACCGGTTGGCTTACACACGCTGCTACAATGCTGAGTGGGTAAATCCCAA | 1200 |
| QY | 1201 | AGCCATCTCAGTTCGGATTGCTCTGCAACTCGAGGCGATCAAGTTGGAATCGGTAGTA | 1260 |
| DB | 1201 | AGCCATCTCAGTTCGGATTGCTCTGCAACTCGAGGCGATCAAGTTGGAATCGGTAGTA | 1260 |
| QY | 1261 | ATCGCGGAGACCATGCGCGGTGAATAGTTCCTGCAACTCGAGGCGATCAAGTTGGAATCGGTAGTA | 1320 |
| DB | 1261 | ATCGCGGAGACCATGCGCGGTGAATAGTTCCTGCAACTCGAGGCGATCAAGTTGGAATCGGTAGTA | 1320 |
| QY | 1321 | ACCATGGAGTGGTTCCTACCGAGCAGCGTACGCTAAGTTCGGGGGACGCGGCCAC | 1380 |
| DB | 1321 | ACCATGGAGTGGTTCCTACCGAGCAGCGTACGCTAAGTTCGGGGGACGCGGCCAC | 1380 |
| QY | 1381 | GSTAGGATCAGCGACTGGGGTGAAGTCTGTAACAGTAGCCGTAGGGGAACCTGCGGCTG | 1440 |
| DB | 1381 | GSTAGGATCAGCGACTGGGGTGAAGTCTGTAACAGTAGCCGTAGGGGAACCTGCGGCTG | 1440 |
| QY | 1441 | GATCACCCTCCTT 1452 | |
| DB | 1441 | GATCACCCTCCTT 1452 | |

RESULT 5

AAQ81791
ID AAQ81791 standard; DNA; 1451 BP.

XX AAQ81791;

XX AC

XX XX

XX 25-MAR-2003 (updated)

XX 15-SEP-1995 (first entry)

XX DE

XX Nucleotide sequence encoding 16S rRNA of new bacterium strain E-396.

XX 16S ribosomal RNA; rRNA; carotenoid pigment; astaxanthin;

XX adonixanthin; beta-carotene; production; novel bacterium;

XX industrial application; ds.

XX new genus, strain E-396 (FERM BP-4283).

OS EP635576-A1.

XX 25-JAN-1995.

XX 22-JUL-1994; 94EP-0111525.

XX 22-JUL-1993; 93JP-0181615.

XX (NIOC) NIPPON OIL KK.

PA

PA (NIOC) NIPPON OIL CO LTD.
 XX Kiyota T, Takaki M, Tsubokura A, Yoneda H;
 XX WPI; 1995-053688/08.
 XX New bacteria which produce carotenoid pigments - used for the
 PT prodn. of astaxanthin, adonixanthin, beta-carotene, echinenone,
 PT canthaxanthin and zeaxanthin
 XX
 PS Disclosure; Page 20-21; 29pp; English.
 XX
 CC This DNA sequence encodes a 16S rRNA isolated from a new genus of
 CC bacteria, designated E-396. This bacterium is capable of producing
 CC carotenoid pigments selected from astaxanthin, adonixanthin, beta-
 CC carotene, etc. The carotenoid pigments can be produced in industrial
 CC quantities and used for feed additives.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 1451 BP; 353 A; 346 C; 460 G; 291 T; 1 other;
 Query Match 99.1%; Score 1439; DB 16; Length 1451;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1451; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 AGTTTGATCTCGGCTCAGAACGACGCTGGCGGAGGCTTAACACATGCAAGTCGAGCGA 60
 DB 1 AGTTTGATCTCGGCTCAGAACGACGCTGGCGGAGGCTTAACACATGCAAGTCGAGCGA 60
 QY 61 GACCTTCGGGCTAGCGCGGACGCGGTGAGTAACGCGTGGGACGTCCTCTCTACGG 120
 DB 61 GACCTTCGGGCTAGCGCGGACGCGGTGAGTAACGCGTGGGACGTCCTCTCTACGG 120
 QY 121 AATAGCCCGGGAACCTGGAGTAATACCGTATAGCCCTTGGGGGAAAGATTATCGG 180
 DB 121 AATAGCCCGGGAACCTGGAGTAATACCGTATAGCCCTTGGGGGAAAGATTATCGG 180
 QY 181 AGAAGGATCGCCCGGCTTGGATTAGTGTGGGTATGGCCCAACCAAGCCGACG 240
 DB 181 AGAAGGATCGCCCGGCTTGGATTAGTGTGGGTATGGCCCAACCAAGCCGACG 240
 QY 241 ATCCATAGCTGGTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTC 300
 DB 241 ATCCATAGCTGGTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTC 300
 QY 301 CTACGGGAGGACGAGTGGGAATCTTAGACAATGGGGCAACCCCTGATCTAGCCATGCC 360
 DB 301 CTACGGGAGGACGAGTGGGAATCTTAGACAATGGGGCAACCCCTGATCTAGCCATGCC 360
 QY 361 GCGTGAGTGATGAAGGCTTAGGGTTGTAAAGCTCTTTCAGCTGGGAAGATAATGACGGT 420
 DB 361 GCGTGAGTGATGAAGGCTTAGGGTTGTAAAGCTCTTTCAGCTGGGAAGATAATGACGGT 420
 QY 421 ACCAGCAGAAGACCGCGGCTAATCTCGTGCCAGCAGCCGCGGTAAATACGGAGGGGCT 480
 DB 421 ACCAGCAGAAGACCGCGGCTAATCTCGTGCCAGCAGCCGCGGTAAATACGGAGGGGCT 480
 QY 481 AGCGTGTCTCGGAATTAATCTGGGCTTAAGCCGACGCTAGGCGGACTGGAAGTCAGAGGTG 540
 DB 481 AGCGTGTCTCGGAATTAATCTGGGCTTAAGCCGACGCTAGGCGGACTGGAAGTCAGAGGTG 540
 QY 541 AAATCCAGGCGCTCAACCTTGGAACTGCTTTGAACTATCAGTCTGGAGTTCGAGAGAG 600
 DB 541 AAATCCAGGCGCTCAACCTTGGAACTGCTTTGAACTATCAGTCTGGAGTTCGAGAGAG 600
 QY 601 GTGAGTGAATTCGAGGTGAGAGTGAATTCGTAGATATTCGAGGAAACACCAAGTGGC 660
 DB 601 GTGAGTGAATTCGAGGTGAGAGTGAATTCGTAGATATTCGAGGAAACACCAAGTGGC 660
 QY 661 GAAGCGGCTCAGTGGCTCGATGACTGACCGCTGAGGTGCGGAAGCGTGGGAGCAACAGG 720
 DB 661 GAAGCGGCTCAGTGGCTCGATGACTGACCGCTGAGGTGCGGAAGCGTGGGAGCAACAGG 720

QY 721 ATTAGATACCCTGGTAGTCCACGCGTAAACGATGAATGCCAGAGTCGCGAAGCATGCT 780
 DB 721 ATTAGATACCCTGGTAGTCCACGCGTAAACGATGAATGCCAGAGTCGCGAAGCATGCT 780
 QY 781 TGTGGTGTACACCTAACCGATTAAAGCATTCGCCCTGGGAGTACGCTCGCAAGATTAA 840
 DB 781 TGTGGTGTACACCTAACCGATTAAAGCATTCGCCCTGGGAGTACGCTCGCAAGATTAA 840
 QY 841 AACTCAAGGAATTGACGGGGCGCCGACACGCGGTGAGCATGTGGTTTAAATTCGAAGC 900
 DB 841 AACTCAAGGAATTGACGGGGCGCCGACACGCGGTGAGCATGTGGTTTAAATTCGAAGC 900
 QY 901 AACCGGAGAACCTTACCAACCTTGACATGGCAGGACCGCTGGAGAGATTTCAGCTTTCT 960
 DB 901 AACCGGAGAACCTTACCAACCTTGACATGGCAGGACCGCTGGAGAGATTTCAGCTTTCT 960
 QY 961 CGTAAGAGACCTGCACACAGGTGCTGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 DB 961 CGTAAGAGACCTGCACACAGGTGCTGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 QY 1021 GGTAAAGTCCGGACGAGCGCAACCCACGCTCCCTAGTTGCCAGCAATTCAGTTGGGAC 1080
 DB 1021 GGTAAAGTCCGGACGAGCGCAACCCACGCTCCCTAGTTGCCAGCAATTCAGTTGGGAC 1080
 QY 1081 TCTATGGAACCTGCCGATGATAAGTCGGAGGAAGGTGTGGATGAGTCAAGTCCCTCATGG 1140
 DB 1081 TCTATGGAACCTGCCGATGATAAGTCGGAGGAAGGTGTGGATGAGTCAAGTCCCTCATGG 1140
 QY 1141 GCCTTACGGGTTGGGCTACACAGCTGTACAATGTGTGTGACAGTGGGTTAATCCCAAA 1200
 DB 1141 GCCTTACGGGTTGGGCTACACAGCTGTACAATGTGTGTGACAGTGGGTTAATCCCAAA 1200
 QY 1201 AGCCATCTCAGTTCGGATTGCTCTGCAACTCGAGGCGATGAAGTTGGAATCGTAGTA 1260
 DB 1201 AGCCATCTCAGTTCGGATTGCTCTGCAACTCGAGGCGATGAAGTTGGAATCGTAGTA 1260
 QY 1261 ATCGCGGAACAGCATGCCGCGTGAATACGTTCGCGGCGCTTGTACACACCGCCGCTCAC 1320
 DB 1261 ATCGC-GAAGACGATGCCGCGTGAATACGTTCGCGGCGCTTGTACACACCGCCGCTCAC 1320
 QY 1321 ACCATGGAGTGGTTCTTACCGGACGAGTGGCTAAGCTTCGCGGCGGAGCGGCCAC 1380
 DB 1321 ACCATGGAGTGGTTCTTACCGGACGAGTGGCTAAGCTTCGCGGCGGAGCGGCCAC 1380
 QY 1381 GGTAGGATCAGGACTGGGGTGAAGTCGTAACAGGTAGCCGTAGGGAACCTGCGGCTG 1440
 DB 1381 GGTAGGATCAGGACTGGGGTGAAGTCGTAACAGGTAGCCGTAGGGAACCTGCGGCTG 1440
 QY 1441 GATCACTCTCTT 1452
 DB 1440 GATCACTCTCTT 1451
 RESULT 6
 AAX07384
 ID AAX07384 standard; RNA; 1430 BP.
 XX AAX07384;
 AC AAX07384;
 XX 07-JUN-1999 (first entry)
 DT
 XX Paracoccus marcusii 16S rRNA gene.
 DE
 XX Carotenoid; beta-carotene; echinenone; canthaxanthin;
 KW beta-cryptoxanthin; adonirubin; cis-adonixanthin;
 KW astaxanthin; zeaxanthin; pigment; ds.
 XX
 OS Paracoccus marcusii.
 XX
 PW W09906586-Al.
 XX
 PD 11-FEB-1999.
 XX

PF 16-JUL-1998; 98WO-US14905.
 XX 29-JUL-1997; 97US-0902618.
 XX (FRIE/) FRIEDMAN M M.
 PA (YISS) YISSUM RES & DEV CO.
 XX Harkar M., Hirschberg J;
 PI WPI; 1999-153810/13.
 XX New Paracoccus marcusii bacterium that produces and secretes
 PT carotenoid pigments - useful, as additives for animal feeds or human
 PT foods, in cosmetics and as pharmaceuticals
 XX Disclosure; Page 40-41; 55pp; English.
 XX This is the nucleotide sequence of the 16S ribosomal RNA gene of
 CC Paracoccus marcusii type strain DSM 11574 (also named Paracoccus
 CC strain WH1). The 16S rRNA gene can be used to identify this novel
 CC Paracoccus species. P. marcusii appeared as a single orange colony
 CC contaminating a nutrient agar plate. It produces and secretes
 CC carotenoids such as beta-carotene, echinenone, beta-cryptoxanthin,
 CC canthaxanthin, adonirubin, cis-adonixanthin, adonixanthin,
 CC astaxanthin and zeaxanthin in vesicles. A process for producing
 CC beta-carotenoids comprising culturing P. marcusii DSM 11574 in a
 CC nutrient medium including sources of carbon, nitrogen and inorganic
 CC substances, and recovering an individual carotenoid pigment or a
 CC mixture of carotenoid pigments from cells, vesicles and/or medium.
 CC The carotenoids are useful as additives for human foods or animal
 CC feeds (e.g. in salmonid fish farming) or cosmetics, and
 CC beta-carotene is used as a pharmaceutical. The new bacterium
 CC provides a ready source of carotenoids that are currently very
 CC expensive to synthesise or to extract from natural sources.
 XX Sequence 1430 BP; 349 A; 343 C; 456 G; 282 U; 0 other;
 SQ

Query Match 97.4%; Score 1414.8; DB 20; Length 1430;
 Best Local Similarity 80.0%; Pred. No. 0;
 Matches 1145; Conservative 282; Mismatches 3; Indels 1; Gaps 1;

QY 16 CAGACGACGCTGGCGGAGGCTTAACATCAAGTCGAGGAGACCTTCGGGTCTAG 75
 DB 1 CAGACGACGCTGGCGGAGGCTTAACATCAAGTCGAGGAGACCTTCGGGTCTAG 60
 QY 76 CGCGGACGCGGTGAGTAACGCGTGGGAACGTCGCTTCTCTACGGAATAGCCCGGAAA 135
 DB 61 CGCGGACGCGGTGAGTAACGCGTGGGAACGTCGCTTCTCTACGGAATAGCCCGGAAA 120
 QY 136 CTGGGAGTATACGCTATAGCCCTTTGGGGGAAAGATTATTCGGAGAAAGATCGGCCG 195
 DB 121 CUGGGAGUAUACCGUAUACGCCCUUUGGGGAAAGUAUUAUCGGAGAAUCGCGCCG 180
 QY 196 CGTTGATTAGGTAGTGTGGGTATGTCGCCCAAGCGAGCTCCATAGTGTGTTT 255
 DB 181 CGUUGUAUAGGUAUUGGUGGUAUUGGCCCAAGCGAGCCGAGUCCAUAGCUGGUU 240
 QY 256 GAGAGGATGATCAGCCACACTGGGACTGAGACAGCGGCCAGCTCTACGGGAGGACGA 315
 DB 241 GAGAGGUAUACGACACACGUGGACUGAGACAGCGGCCAGACUCCUACGGGAGGACGA 300
 QY 316 GTGGGAAUATTAGACAAATGGGGCAACCTGTATAGCCATCGCGGTGAGTGAAG 375
 DB 301 GUGGGAAUUAUAGAAUUGGGGCAACCCUGAUUAGCCUAGCCUAGCGGUGAGUAGAAG 360
 QY 376 GCCTTAGGTTGTAAGCTTTTACGCTGGGAGATATACGCTACCAAGAGGAC 435
 DB 361 GCCUUGAGGUGUUAAGCUCUUCAGCUGGGAGUAUUAUAGCCGACCAAGAGGAC 420
 QY 436 CCGGGTAACTCCGTGACGACGCGCGGTAAATACGAGGGGGGTACGCTTGTTCGAAT 495
 DB 421 CCGGGUACUCCGUGCCACGACGCGCGGUAUUAUAGCGAGGGGGGCUAGCGUUGCGAAU 480

QY 496 TACTGGCGCTAAAGCGACGCTAGCGAGCTGGAAGTCAGAGGTGAATCCAGGGCTCA 555
 DB 481 UACUGGGCGUAAAGCGACGAGCGGACUGGAGAAAGUCAGAGGUAUUAUCCAGGGCUCA 540
 QY 556 ACCTTGGAACCTGCTTTGAAACATATCAGTCTGAGTTCGAGAGAGTGTGAGTGAATCCG 615
 DB 541 ACCUUGGAACUGCCUUUUAACUACUAGUCUGAGUUCGAGAGGUGAGUGAAUCCG 600
 QY 616 AGTGTAGAGGTGAATTCGTAGATATTCGAGGAAACACACAGTGTGCGAGGCGGTCACTG 675
 DB 601 AGUGAGAGGUGAAAUUUCGUAGAUUUCGAGGAAACACACAGTGTGCGAGGCGGTCACTG 660
 QY 676 GCTCGATACGACGCTGAGTGTGAGAGCGTGGGAGCAACAGGATTAGATACCTCGGT 735
 DB 661 GCUCGUAUCGACGUGAGGUGGAAAGCGGAGGAGCAACAGGAAUUAUACCCUUGG 720
 QY 736 AGTCCAGCGCGCTAAACGATGAATGCCAGAGCTCGGCAAGCATGTTCTCGGTGTACACC 795
 DB 721 AGUCCAGCGCGUAAACGUAUAGUCCAGACGCGGCAAGCAUGCUUCGUGGUCACACC 780
 QY 796 TAACGGATTAAAGATTCGCGCTGGGAGTACGCTGCGCAAGATTAAACTCAAGGAATTG 855
 DB 781 UAAACGAAUUAAGCAUUCGCGGAGAGACGCGGAGCAAGAAUUAUAAACUCAAAGGAUUG 840
 QY 856 ACGGGGCGCGCACAGCGTGGAGCATGTGTTTAAATTCGAAGCAGCGCAGAACCTT 915
 DB 841 ACGGGGCGCGCACAGCGTGGAGCATGTGTTTAAATTCGAAGCAGCGCAGAACCTT 900
 QY 916 ACCAACCTTGAACATGCGAGGACCGCTGGAGAGATTCAAGTCTTCTCTAGAGACCTGCA 975
 DB 901 ACCAACCTTGAACATGCGAGGACCGCTGGAGAGATTCAAGTCTTCTCTAGAGACCTGCA 960
 QY 976 CACAGTGTGCTGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1035
 DB 961 CACAGTGTGCTGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
 QY 1036 CGAGCGCAACCCAGCTCCCTAGTGTGCCAGCAATTCAGTGGGAATCTATGGAACCTGCC 1095
 DB 1021 CGAGCGCAACCCAGCTCCCTAGTGTGCCAGCAATTCAGTGGGAATCTATGGAACCTGCC 1079
 QY 1096 GATGATAAGTCGGAGGAGGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1155
 DB 1080 GAUGAUAUAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1139
 QY 1156 CTACACAGTGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1215
 DB 1140 CUACACAGGUGUACAAUUGGUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1199
 QY 1216 GATTGTCTCTGCAACTCGAGGGGATGAGTGTGGAATCGCTAGTAAATCGCGGAAACAGCAT 1275
 DB 1200 GAUUGUCCUUGCAACUCCGAGGGGCAUGAUGGUAUUGGUAUUGGUAUUGGUAUUGGUA 1259
 QY 1276 GCGCGGTGATAGCTTCCCGGGCTTGTACACACCCCGCTCACACATGAGGAGTGTGTT 1335
 DB 1260 GCGCGGUAUAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1319
 QY 1336 TCTACCGGACGAGCAGTGGCTTAACCTTTCGGGGGAGGAGGAGGAGGAGGAGGAGGAGG 1395
 DB 1320 UCUACCGGACGAGCAGGUGGUAUACCUUCGCGGGGAGGAGGAGGAGGAGGAGGAGGAGG 1379
 QY 1396 TGGGGTAACTCGTAACAGGTAGCCCTGAGGGAACCTGCGGCTGGATCAC 1446
 DB 1380 UGGGGGUAUAGGUAUAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1430

RESULT 7
 ABL40152
 ID - ABL40152 standard; DNA; 1426 BP.
 XX ABL40152;
 XX AC
 XX AC
 DT 18-MAY-2002 (first entry)
 XX

DE 16S ribosomal RNA from unknown organism A-581-1 DNA sequence SEQ ID NO:2.
XX
KW 16S ribosomal RNA; carotenoid pigment; microbial; carotenoid; pigment;
KW feed additive; food additive; pharmaceutical; gene; ss.
XX
OS Unidentified.
XX
PN WO200196591-A1.
XX
PD 20-DEC-2001.
XX
PF 08-JUN-2001; 2001WO-JF04874.
XX
PR 12-JUN-2000; 2000JP-0175124.
XX
PA (NIOC) NIPPON MITSUBISHI OIL CORP.
XX
PI Tsubokura A, Mizuta H;
XX
DR WPI; 2002-122220/16.
XX
PT Microbial production of carotenoid pigments at varying ratios by
PT controlling concentration of oxygen dissolved in liquid culture medium,
PT useful in feed additives, food additives and pharmaceuticals
XX
PS Disclosure; Page 19; 23pp; Japanese.
XX
CC The present invention describes a microbial method for producing
CC carotenoid compounds at a specified, or varying, ratio by controlling
CC the concentration of oxygen dissolved in the liquid medium during
CC culture. The produced carotenoids are natural pigments, which are useful
CC in feed additives, food additives and pharmaceuticals. The ratio of the
CC carotenoid compounds obtained can be controlled by varying the
CC concentration of oxygen dissolved in liquid medium during culture.
CC The present sequence represents a 16S ribosomal RNA gene from an unknown
CC organism designated A-581-1 which is given in the exemplification of the
CC present invention.
XX
SQ Sequence 1426 BP; 349 A; 342 C; 451 G; 284 T; 0 other;
Query Match 95.0%; Score 1380; DB 24; Length 1426;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1409; Conservative 0; Mismatches 11; Indels 3; Gaps 2;
QY 1 AGTTTGATCCTGGCTCAGAACGACGCTGGCGCAGGCTTAACACATGCAAGTCAGCGA 60
DB 4 AGTTTGATCCTGGCTCAGAACGACGCTGGCGCAGGCTTAACACATGCAAGTCAGCGA 63
QY 61 GACCTTCGGGTCTAGCGCGGACGGGTGAGTAAACGCGTGGGAACGTCCTCTACGG 120
DB 64 GACCTTCGGGTCTAGCGCGGACGGGTGAGTAAACGCGTGGGAACGTCCTCTACGG 123
QY 121 AATAGCCCGGAACTGGGAGTAAATACCGTATACGCCCTTTGGGGAAGATTATCGG 180
DB 124 AATAGCCCGGAACTGGGAGTAAATACCGTATACGCCCTTTGGGGAAGATTATCGG 183
QY 181 AGAAGATCGGCCCGCGTTGGATTAGGTAGTTGGTGAATAGGCCACCAAGCCGACG 240
DB 184 AGAAGATCGGCCCGCGTTGGATTAGGTAGTTGGTGAATAGGCCACCAAGCCGACG 243
QY 241 ATCCATAGTGTGTTGAGAGGATGATCACCACACTGGGACGTAGACAGCGGCCAGACTC 300
DB 244 ATCCATAGTGTGTTGAGAGGATGATCACCACACTGGGACGTAGACAGCGGCCAGACTC 303
QY 301 CTACGGGAGGACGAGTGGGGAATCTTACACAAATGGGCAACCCCTGATCTAGCCATGCC 360
DB 304 CTACGGGAGGACGAGTGGGGAATCTTACACAAATGGGCAACCCCTGATCTAGCCATGCC 363
QY 361 GCGTGAGTGATGAAGCCCTTAGGGTTGTAAGCTCTTTCAGCTGGGAAGATTAATGACGGT 420
DB 364 GCGTGAGTGATGAAGCCCTTAGGGTTGTAAGCTCTTTCAGCTGGGAAGATTAATGACGGT 423
QY 421 ACCAGCAGAAGAGCCCGGCTTAATCTCGTCCGACAGCGCCGGTAAATACGAGGGGGCT 480

DB 424 ACCAGCAGAAGAGCCCGGCTAACTCCGTCCAGCAGCGCGGTAAATACGAGGGGGCT 483
QY 481 AGCGTTGTTCCGGAATTTACTGGCGTAAAGCGCAGCAGTAGGCGGACTGGAAGTCCAGAGGTG 540
DB 484 AGCGTTGTTCCGGAATTTACTGGCGTAAAGCGCAGCAGTAGGCGGACTGGAAGTCCAGAGGTG 543
QY 541 AAATCCAGGGCTCAACCTTTGGAATGCTTTTGAATACTATCACTCTGGAGTTCCAGAGAG 600
DB 544 AAATCCAGGGCTCAACCTTTGGAATGCTTTTGAATACTATCACTCTGGAGTTCCAGAGAG 603
QY 601 GTGAGTGGAAATCCCGAGTGTAGAGGTGAATTCGTAGATATTCGGAGGACACCACTGGC 660
DB 604 GTGAGTGGAAATCCCGAGTGTAGAGGTGAATTCGTAGATATTCGGAGGACACCACTGGC 663
QY 661 GAAGGGCGCTCACTGGCTCGATACCTGAGGTGCGAAGCGTGGGAGCAAAACAGG 720
DB 664 GAAGGGCGCTCACTGGCTCGATACCTGAGGTGCGAAGCGTGGGAGCAAAACAGG 723
QY 721 ATTAGATACCTTGGTAGTCCACGCCCTAAACGATGAATGCCAGACCTGCGCAAGCATGCT 780
DB 724 ATTAGATACCTTGGTAGTCCACGCCCTAAACGATGAATGCCAGACCTGCGCAAGCATGCT 783
QY 781 TGTGCGTGTACACCTTAACGGATTAAAGCATTCGCCCTGGGAGTACGGTCCGAAGTAA 840
DB 784 TGTGCGTGTACACCTTAACGGATTAAAGCATTCGCCCTGGGAGTACGGTCCGAAGTAA 843
QY 841 AACTAAAGAAATTTGACGGGGCCGCCACAAGCGGTGGAGCATGTGGTTAAATTCGAAGC 900
DB 844 AACTAAAGAAATTTGACGGGGCCGCCACAAGCGGTGGAGCATGTGGTTAAATTCGAAGC 903
QY 901 AACGGCAGAACCTTTACCAACCTTTGACATGCGCAGGACCGCTGGAGAGATTCAGCTTCT 960
DB 904 AACGGCAGAACCTTTACCAACCTTTGACATGCGCAGGACCGCTGGAGAGATTCAGCTTCT 963
QY 961 CGTAAGACACTGACACAGAGGTGCTGCATGGCTGTGTCAGTCTGCTGTGAGATGTTTC 1020
DB 964 CGTAAGACACTGACACAGAGGTGCTGCATGGCTGTGTCAGTCTGCTGTGAGATGTTTC 1023
QY 1021 GGTAAAGTCCGCAAGCAGCGCAACCCAGTCCCTAGTTGGCCAGCAATTCAGTTGGGAAC 1080
DB 1024 GGTAAAGTCCGCAAGCAGCGCAACCCAGTCCCTAGTTGGCCAGC-ATTAGTTGGGCAC 1082
QY 1081 TCTATGGAATGCCGATGATTAAGTCGGAGGAGGTGTGGATGACGCTCAAGTCTCATGG 1140
DB 1083 TCTATGGAATGCCGATGATTAAGTCGGAGGAGGTGTGGATGACGCTCAAGTCTCATGG 1142
QY 1141 GCGTTACGGGTTGGGCTACACAGCTGCTACAATGTTGGTGTGACAGTGGGTTAATCCCAA 1200
DB 1143 CCGTTACGGGTTGGGCTACACAGCTGCTACAATGTTGGTGTGACAGTGGGTTAATCCCAA 1202
QY 1201 AGCCATCTCAGTTGGGATTGCTCTGCAACTCGAGGGCATGAAGTTGGAATCGCTAGTA 1260
DB 1203 AGCCATCTCAGTTGGGATTGCTCTGCAACTCGAGGGCATGAAGTTGGAATCGCTAGTA 1262
QY 1261 ATGCGGGAACAGCATGCCCGGTGAATACGTTTCCCGGGCTTGTACACACCGCCGCTAC 1320
DB 1263 ATGCGGGAACAGCATGCCCGGTGAATACGTTTCCCGGGCTTGTACACACCGCCGCTAC 1322
QY 1321 ACCATGGGAGTTGGTCTTACCCGACGACGTCGCTTAACC--TTCCGGGGGAGGCGGCC 1378
DB 1323 ACCATGGGAGTTGGTCTTACCCGACGACGTCGCTTAACCCTTCGCGGAGGCGGCCG 1382
QY 1379 ACGGTAGGATCAGCGACTGGGTTGAAGTCTGTAACAGGTAGCC 1421
DB 1383 ACGGTAGGATCAGCGACTGGGTTGAAGTCTGTAACAGGTAGCC 1425

RESULT 8
ABL55950
ID ABL55950 standard; DNA; 1462 BP.
XX
AC ABL55950;

| | | | | | |
|--|---|---|------|---|------|
| | D | b | 546 | A A A T C C C A G G G C T C A A C C C T G G A A C T G C C T T T G A A A C T C C C G A T C T T G A G G T C G A G A G | 605 |
| | Q | y | 601 | G T G A G T G G A A T T C C G A G T G T A G A G T G A A A T T C G T A G A T A T T C G G A G G A C A C C A G T G G C | 660 |
| | D | b | 606 | G T G A G T G G A A T T C C G A G T G T A G A G T G A A A T T C G T A G A T A T T C G G A G G A C A C C A G T G G C | 665 |
| | Q | y | 661 | G A A G C C G G C T C A C T G G C T C G A T A C T G A C G C T G A G G T G C G A A A G C G T G G G G A G C A A A C A G G | 720 |
| | D | b | 666 | G A A G C C G G C T C A C T G G C T C G A T A C T G A C G C T G A G G T G C G A A A G C G T G G G G A G C A A A C A G G | 725 |
| | Q | y | 721 | A T T A G A T A C C C T G G T A G T T C C A C G C C G T A A A C A G A T G A A T G C C A G A C G T F C G C A A G C A T G C T | 780 |
| | D | b | 726 | A T T A G A T A C C C T G G T A G T T C C A C G C C G T A A A C A G A T G A A T G C C A G T F C G T C G G C A G C A T G C T | 785 |
| | Q | y | 781 | T G T C G G T T C A C A C C T A A C C G A T T A A C A T T C C G C C T G G G A G T A C G G T C C G A A G A T T A A | 840 |
| | D | b | 786 | G T T C G G T G A C A C A C C T A A C G G A T T A A C A T T C C G C C T G G G A G T A C G C C G C A A G G T T A A | 845 |
| | Q | y | 841 | A A C T C A A A G A A T T G A C G G G G C C G C A A A G C G G T G A C A T G T G T T T A A T T C G A A G C | 900 |
| | D | b | 846 | A A C T C A A A G A A T T G A C G G G G C C G C A A A G C G G T G A C A T G T G T T T A A T T C G A A G C | 905 |
| | Q | y | 901 | A A C G C G C A G A A C C T T A C A A C C C T T G A C A T G G C - A G G A C C G C T G G A G A G A T T C A G C T T T C | 959 |
| | D | b | 906 | A A C G C G C A G A A C C T T A C A A C C C T T G A C A T G G C A T G C G G T T C C A G A G A T G T T C C T T C | 965 |
| | Q | y | 960 | T C G T A A G - A G A C C T G C A C A G G T G T G C A T G G C T G T C A G C T G T G C G T A G A T G T | 1018 |
| | D | b | 966 | A G T T C G C C T G G A T C G C A C A G G T G C T G C A T G G C T G T C G T C A G T C G T G C G T G A G A T G T | 1025 |
| | Q | y | 1019 | T C G G T T A A G T C C G C A C A G C G C A C C C A C G T C C C T A G T T G C C A G C A A T T C A G T T G G G A | 1078 |
| | D | b | 1026 | T C G G T T A A G T C C G C A C A G C G C A C C C A C G T C C C T A G T T G C C A G C - A T T C A G T T G G C | 1084 |
| | Q | y | 1079 | A C T C T A T G A A A C T C C C G A T G A T A A G T C G G A A G G T G T G G A T G A C G T C A A G T C C C T C A T | 1138 |
| | D | b | 1085 | A C T C T A G G G A A C T C C G G T G A T A A G C C G A G A A G G T G T G A T G A C G T C A A G T C C C T C A T | 1144 |
| | Q | y | 1139 | G G C C C T T A C G G T T G G G C T A C A C A C G T G C T A C A A T G G T G G T G A C A G T G G G T T A A T C C C C A | 1198 |
| | D | b | 1145 | G G C C C T T A C G G G T T G G G C T A C A C A C G T G C T A C A A T G G C A G T G G G T T A A T C C C A A | 1204 |
| | Q | y | 1199 | A A A G C C A T C A G T C G G A T T G C C C T G C A A C T C G A G G C A T G A A G T T G G A T C C G T A G | 1258 |
| | D | b | 1205 | A A A G C T C T C A G T T G G A T T G G G G T C T G C A C T G A C C C C A T G A A G T C G G A A T C G C T A G | 1264 |
| | Q | y | 1259 | T A A T C G C G G A A C A G C A T G C C G G T G A A T A C G T T C C C G G C C T T G T A C A C A C C G C C G T C | 1318 |
| | D | b | 1265 | T A A T C G C G T A A C A G C A T G A C C G G T G N A T A C G T T C C G G C C T T G T A C A C A C C G C C G T C | 1324 |
| | Q | y | 1319 | A C A C A T G G G A G T T G G T T C T A C C G A C A G C G N T G C G T A A C C T - - - - T C G G G G G G C A G C | 1374 |
| | D | b | 1325 | A C A C A T G G A A T T G G T T C T A C C G A A G G C G G T G C C C A A C C C T C G A A G A G G A G G A G C C | 1384 |
| | Q | y | 1375 | G G C A C G G T A G G A T C A G C A C T G G G T G A G T C G T A A C A G G T A G C C G T A G G G A A C C T G | 1434 |
| | D | b | 1385 | G A C C A C G G T A G G A T C A G T G A C T G G G G T G A A G T C G T A A C A A G G T A G C C G T A G G G A A C C T G | 1444 |
| | Q | y | 1435 | C G G C T G S A T C A C C T C C T T | 1452 |
| | D | b | 1445 | C G G C T G S A T C A C C T C C T T | 1462 |

RESULT 9
 ABL55996
 ID ABL55996 standard; DNA; 1462 bp.
 XX AC ABL55996;
 XX DT 17-JUN-2002 (first entry)
 XX DE Rhodospseudomonas 16S rDNA SEQ ID NO 4.

| | | |
|----|---|--|
| XX | Rhodopseudomonas; 16S rDNA; photosynthetic; FERM P-17849; | |
| KW | azo dye; decomposing activity; ds. | |
| XX | Rhodopseudomonas sp. | |
| OS | Rhodopseudomonas sp. | |
| XX | JP2002045171-A. | |
| PN | 12-FEB-2002. | |
| XX | | |
| PD | | |
| XX | | |
| XX | 20-DEC*2000; 2000JP-0387555. | |
| PF | | |
| XX | | |
| XX | 26-MAY-2000; 2000JP-0156244. | |
| PR | | |
| XX | (TAIC) TAIYO KAGAKU KOGYO KK. | |
| XX | WPI; 2002-275855/32. | |
| DR | | |
| XX | | |
| XX | New microbe; useful for decomposition of compound | - |
| PT | Disclosure; Page 10; 16pp; Japanese. | |
| XX | | |
| XX | | |
| CC | The invention relates to a photosynthetic microbe, preferably | |
| CC | Rhodopseudomonas FERM P-17849 strain having azo dye-decomposing activity. | |
| CC | The present sequence is that of a Rhodopseudomonas 16S rDNA sequence, | |
| CC | useful to the invention. | |
| XX | | |
| XX | | |
| SQ | Sequence 1462 BP; 356 A; 352 C; 464 G; 290 T; 0 other; | |
| | | |
| | Query Match | 85.88; Score 1246.2; DB 24; Length 1462; |
| | Best Local Similarity | 92.7%; Pred. No. 0; |
| | Matches 1352; Conservative | 0; Mismatches 99; Indels 7; Gaps 4; |
| QY | 1 AGTTTGATCTGCTCAGAACGACGCTGCGCGAGGCTTAACACATGCAAGTCGAGCGA | 60 |
| DB | | |
| DB | 6 AGTTTGATCTGCTCAGAAATGACGCTGCGCGAGGCTTAACACATGCAAGTCGAGCGA | 65 |
| QY | 61 GACCTTCGGGTCTAGCGGCGGACGGGTGAGTAACGCTGGGAAAGTGCCTTCTCTACGG | 120 |
| DB | | |
| DB | 66 AGTCTTCGGACTTAGCGGCGGACGGGTGACTAACGCTGGGAAAGTGCCTTCTCTACGG | 125 |
| QY | 121 AATAGCCCCGGGAAACTGGGAGTAATACCGCTATACGCCCTTTGGGGGAAAGATTTATCGG | 180 |
| DB | | |
| DB | 126 AATAGCCCCGGGAAACTGGGAGTAATACCGAAATGTGCCCTACGCGGGGAAAGATTTATCGG | 185 |
| QY | 181 AGAAGGATCGGCCCGCTTGATTTAGTACTTGTTGGGTGAATGGCCCAACCAAGCCGACG | 240 |
| DB | | |
| DB | 186 CAAGGATCGGCCCGCTTGATTTAGTACTTGTTGGGTGAATGGCCCTACCAAGCCGACG | 245 |
| QY | 241 ATCCATAGCTGTTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGCCCCAGACTC | 300 |
| DB | | |
| DB | 246 ATCCATAGCTGTTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGCCCCAGACTC | 305 |
| QY | 301 CTACGGGAGCAGCTAGGGGATCTTAGACATGGGGCAACCCCTGATCTAGCCATGCC | 360 |
| DB | | |
| DB | 306 CTACGGGAGCAGCTAGGGGATCTTAGACATGGGGCAACCCCTGATCTAGCCATGCC | 365 |
| QY | 361 GCGTGAGTGATGAAGGCCCTTAGGGTTGTAAAGCTCTTTACGCTGGGAAGATAATGACGGT | 420 |
| DB | | |
| DB | 366 GCGTGATGATGAAGGCCCTTAGGGTTGTAAAGATCTTTACGCTGGGAAGATAATGACGGT | 425 |
| QY | 421 ACCAGCAGAAGAGCCCCGGCTAACTCCGTGCCAGCAGCCGCGGTAAATACGGAGGGGCT | 480 |
| DB | | |
| DB | 426 ACCACCAGAAGAGCCCCGGCTAACTCCGTGCCAGCAGCCGCGGTAAATACGGAGGGGCT | 485 |
| QY | 481 AGCGTTTTCGGAAATTAATGCGGCGTAAGCGACGCTAGCGCGACTGGAAGTACAGAGTG | 540 |
| DB | | |
| DB | 486 AGCGTTTATTCGGAATTAATGCGGCGTAAGCGACGCTAGCGCGACTGGAAGTACAGAGTG | 545 |
| QY | 541 AATATCCAGGGCTCAACCTGGAACTGCCTTTTGAACATCATCTCTGGAGTTCGAGAGAG | 600 |
| DB | | |
| DB | 546 AATATCCAGGGCTCAACCTGGAACTGCCTTTTGAACATCCCGATCTCTGGAGTTCGAGAGAG | 605 |

| | | | |
|------|----|--|------|
| 601 | QY | GTGAGTGGAAATCCGAGGTGAGAGTGAATTCGTAGATATTCGGAGGAACACCAAGTGGC | 660 |
| 606 | Db | | 665 |
| 661 | QY | GTGAGTGGAAATCCGAGGTGAGAGTGAATTCGTAGATATTCGGAGGAACACCAAGTGGC | 720 |
| 666 | Db | | 725 |
| 721 | QY | GAAGGGGGCTCACTGGCTCGATACTGACGCTGAGGTGCGAAGCGGTGGGAGCAACACAGG | 780 |
| 726 | Db | | 785 |
| 781 | QY | ATTAGATACCTCGTGTAGTCCACCGGTAAACGATGAATGCCACACGCTCGGCAAGCATGCT | 840 |
| 786 | Db | | 845 |
| 841 | QY | ATCTCAAGAAATTGACGGGGGGCCCGCACAGCGGTGGAGCATGTGGTTTAATTCGAAGC | 900 |
| 846 | Db | | 905 |
| 901 | QY | AACGCGCAGAACCTTACCAACCCCTTGACATGGC - AGGACGCGTGGAGAGATTTCAGCTTTC | 959 |
| 906 | Db | | 965 |
| 960 | QY | TCGTAAG - AGACCTTGACACACAGTGTGTCATGGCTGTCGTACGCTGCTGTGAGATGT | 1018 |
| 966 | Db | | 1025 |
| 1019 | QY | TCGGTTAAGTCCGGCAACGAGCGCAACCCACGTCCCTAGTTGCCAGCAATTCAGTTGGGA | 1078 |
| 1026 | Db | | 1084 |
| 1079 | QY | ACTCTATGAAACTGCCGATGATAAGTCGGAGGAAGGTGGATGACGTCAAGTCCCTCAT | 1138 |
| 1085 | Db | | 1144 |
| 1139 | QY | GGCCCTTACGGGTTGGGCTACACACGTGCTACAAATGGTGGTGACAGTGGGTTAATCCCCA | 1198 |
| 1145 | Db | | 1204 |
| 1199 | QY | AAAGCCATCTCAGTTCGGATTGCTCTGCAACTCGAGGGCATGAAGTTGGAATTCGCTAG | 1258 |
| 1205 | Db | | 1264 |
| 1259 | QY | TAATCGGGNACAGCATCGCCGGTGAAATACGTTCCGGGCCCTTGTACACACCGCCGCTC | 1318 |
| 1265 | Db | | 1324 |
| 1319 | QY | ACACCTGGAGTTGGTTCTTACCCGACGACGNTGCGCTAACCT - ---TCGGGGGGGAGGC | 1374 |
| 1325 | Db | | 1384 |
| 1375 | QY | GGCCACGGTAGGATACAGCACTGGGTGGAAGTCGTAAACAGGTAGCCGTAGGGGAACCTG | 1434 |
| 1385 | Db | | 1444 |
| 1435 | QY | CGGCTGGATCACCTCCTT | 1452 |
| 1445 | Db | | 1462 |

RESULT 10

AAX03559
ID AAX03559 standard; DNA; 1426 BP.

AC . AAX03559;

DT 08-APR-1999 (first entry)

DE Nucleotide sequence encoding 16s rRNA of *Paracoccus* genus.

KW Selenic acid; microbe; Paracoccus; 6-valent selenium; reduction;
 KW waste water treatment; 16S rRNA; ss.

XX OS Paracoccus sp.
 XX PN JP10309190-A.
 XX PD 24-NOV-1998.
 XX PF 09-MAY-1997; 97JP-0136157.
 XX PR 09-MAY-1997; 97JP-0136157.
 XX PA (MITO) MITSUBISHI JUKOGYO KK.
 XX PS WPI; 1999-073901/07.
 XX PT New selenic acid reducing microbe, Paracoccus genus - useful in
 PT removing selenium in waste water treatment
 XX Examples; Fig 5, 6; 13pp; Japanese.
 XX The invention relates to a selenic acid reducing microbe FERM BP-5662
 CC that belongs to Paracoccus genus. It has the ability of reducing 6-valent
 CC selenium (Se). Also provided is a method for waste water treatment
 CC comprising removing Se from waste water by reducing Se from 6-valent to
 CC 4-valent (optionally to an Se simple substance) by microbe (as above)
 CC treatment on the active sludge to separate the solid from the liquid.
 CC The microbe is useful in water treatment to remove (6-valent) selenium.
 CC The microbe is more efficient at removing 6-valent selenium than the
 CC prior art methods. The present sequence represents the nucleotide
 CC sequence of 16S rRNA that is used in the method of the invention.
 XX
 XX Sequence 1426 BP; 349 A; 316 C; 477 G; 284 T; 0 other;
 Query Match 85.7%; Score 1244.4; DB 20; Length 1426;
 Best Local Similarity 93.0%; Pred. No. 0;
 Matches 1325; Conservative 0; Mismatches 97; Indels 3; Gaps 2;
 QY 1 AGTTGATCTGCTCAGACGACGCTGGCGGAGCTTAACACATGCAAGTCGACGA 60
 DB 3 AGTTGATCTGCTCAGACGACGCTGGCGGAGCTTAACACATGCAAGTCGACGA 62
 QY 61 GACCTTCGGGTCTAGCGGCGGAGTGTAGTACGCTGGGAGAGTCCCTTCTCTACGG 120
 DB 63 ACCCTTCGGGTCTAGCGGCGGAGTGTAGTACGCTGGGAGAGTCCCTTCTCTACGG 122
 QY 121 AATAGCCCCGGGAACTGGGAGTAATACCTATACGCCCTTTGGGGGAAAGATTATCGG 180
 DB 123 AATAGCCCCGGGAACTGGGAGTAATACCTATACGCCCTTTGGGGGAAAGATTATCGG 182
 QY 181 AAGAGGATCGGCCGCTTGGATTAGTGTAGTGGGGTAAATGGGCCCAACAGCCGACG 240
 DB 183 CAAGGATTAGCCCGGCTTGGATTAGTGTAGTGGGGTAAATGGGCCCAACAGCCGACG 242
 QY 241 ATCATAGCTGTTTGGAGAGTATCATGACACACATGGGAGTGGAGACGCGCCAGACTC 300
 DB 243 ATCATAGTGTGTTGAGAGATGATCAGCCACATGGGAGTGGAGACGCGCCAGACTC 302
 QY 301 CTACGGGAGCAGAGTGGGGAATCTTAGACAATGGGGCAACCCCTGATCTAGCCATGCC 360
 DB 303 CTACGGGAGCAGAGTGGGGAATCTTAGACAATGGGGCAACCCCTGATCTAGCCATGCC 362
 QY 361 CGGTGATGATGAAGGCTTAGGTTGTAAGCTCTTTCAGCTGGGGAAGATATGACGGT 420
 DB 363 CGGTGATGATGAAGGCTTAGGTTGTAAGCTCTTTCAGCTGGGGAAGATATGACGGT 422
 QY 421 ACCAGCAGAGAGAGCCCGGCTACTCCGTGCCAGCAGCCCGGTATATAGGAGGGGCT 480
 DB 423 ACCAGCAGAGAGAGCCCGGCTACTCCGTGCCAGCAGCCCGGTATATAGGAGGGGCT 482
 QY 481 AGCGTTTCTCGGAATTACTGGCGTAAGCGCAGTACGAGGGGAGTGGGAAGTTCAGAGGTG 540
 DB 483 AGCGTTTCTCGGAATTACTGGCGTAAGCGCAGTACGAGGGGAGTGGGAAGTTCAGAGGTG 542

QY 541 AATCCAGGGCTCAACCTTGGAACTGCCTTTGAACTATCAGTCTGGAGTTCGAGAGAG 600
 DB 543 AATCCAGGGCTCAACCTTGGAACTGCCTTTGAACTATCAGTCTGGAGTTCGAGAGAG 602
 QY 601 GTGAGTGAATTCGGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAAACACCGATGGC 660
 DB 603 GTGAGTGAATTCGGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAAACACCGATGGC 662
 QY 661 GAAGGGGCTCACTGGCTGCTAGTACGCTGAGGTGGAAGCTGGGAGGAAACAGG 720
 DB 663 GAAGGGGCTCACTGGCTGCTAGTACGCTGAGGTGGAAGCTGGGAGGAAACAGG 722
 QY 721 ATTAGATACCTGTGAGTCCAGCGCTAAACGATGAATGCCAGACGTCGGCAACATGCT 780
 DB 723 ATTAGATACCTGTGAGTCCAGCGCTAAACGATGAATGCCAGACGTCGGCAACATGCT 782
 QY 781 TGTGCGGTGCACACCTAACCGATTAAAGCATTCGCGCTGGGAGTACGGTTCGCAAGATTAA 840
 DB 783 GTTCGGTGCACACCTAACCGATTAAAGCATTCGCGCTGGGAGTACGGTTCGCAAGATTAA 842
 QY 841 AACTCAAGGAATTGACGGGGGCGGCACAAAGCGGTGAGCATGTGTTTAAATTCGAGC 900
 DB 843 AATCAAGGAATTGACGGGGGCGGCACAAAGCGGTGAGCATGTGTTTAAATTCGAGC 902
 QY 901 AACGCGCAGAACCTTACCAACCTTGACATGGCAGGACCGCTGGAGAGATTACGCTTCT 960
 DB 903 AACGCGCAGAACCTTACCAACCTTGACATGGCAGGACCGCTGGAGAGATTACGCTTCT 962
 QY 961 CGTAAGAGACCTGCACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 DB 963 GGTAAAGAGACCTGTGGACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1022
 QY 1021 GGTAAAGAGACCTGTGGACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 DB 1023 GGTAAAGAGACCTGTGGACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1081
 QY 1081 TCTATGAAACTGCGGATGATAGTTCGAGGAGAGTGTGGATGACGTCAGTCTCATGG 1140
 DB 1082 TCTAAGAGAACTGCGGATGATAGTTCGAGGAGAGTGTGGATGACGTCAGTCTCATGG 1141
 QY 1141 GCCTTACGGTGGGCTTACACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 DB 1142 GCGTTAGGGTGGGCTTACACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1201
 QY 1201 AGCATCTCAGTTCGGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
 DB 1202 AGCATCTCAGTTCGGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1261
 QY 1261 ATCGCGAAGACAGATGCGCGGTGAATACGTTCCCGGCTTGTACACACCGCGCTCAC 1320
 DB 1262 ATCGCGAAGACAGATGCGCGGTGAATACGTTCCCGGCTTGTACACACCGCGCTCAC 1321
 QY 1321 ACCATGGAGTGGTCTTACCGGACGAGTTCGCTTACCTTC--GGGGGCGAGCGCGCC 1378
 DB 1322 ACCATGGAGTGGTCTTACCGGACGAGTTCGCTTACCTTC--GGGGGCGAGCGCGCC 1381
 QY 1379 ACGGTAGATCAGCAGTGGGGTGAAGTTCGTAACAGTAGCCGT 1423
 DB 1382 ACGGTAGATCAGCAGTGGGGTGAAGTTCGTAACAGTAGCCGT 1426

RESULT 11

AAH48039
 ID AAH48039 standard; DNA; 1407 BP.

XX AC AAH48039;

XX AC AC

XX DT 18-SEP-2001 (first entry)

XX DE Oligonucleotide SEQ ID 1.

XX KW Beta-hydroxybutyric acid; PHB; waste water treatment; ds.

OS Paracoccus kawasakienis.
 PN JP200115483-A.
 XX 29-MAY-2001.
 XX 19-NOV-1999; 99JP-0330419.
 XX 19-NOV-1999; 99JP-0330419.
 PR (BIOI-)*BIOINDUSTRY KYOKAI SH.
 PA (AJIN) AJINOMOTO KK.
 PA (KEIZAI) KEIZAI SANGYOUSHO SANGYO GIUTSU SOGO KEN.
 XX WPI; 2001-387291/41.
 DR
 XX
 XX A new microorganism Paracoccus kawasakienis is used for treatment of
 PT waste water and production of beta-hydroxybutyric acid -
 PT
 XX Disclosure; Page 4; 5pp; Japanese.
 PS
 CC The present invention relates to a new beta-hydroxybutyric acid producing
 CC microorganism Paracoccus kawasakienis (FERM P-17644, Bp-7059). The new
 CC microorganism has properties of Paracoccus sp., is unable to grow in a
 CC medium containing 0.3% or more of sodium chloride, unable to assimilate
 CC potassium nitrate or glutamic acid, but is able to assimilate ammonium
 CC sulphate as a nitrogen source. Also, the microorganism has urease
 CC activity, but is unable to assimilate xylose, mannitol, maltose or
 CC lactose. The microorganism is able to assimilate arabinose and sucrose as
 CC sole carbon sources. The microorganism is useful for the production of
 CC beta-hydroxybutyric acid (PHB) and treatment of waste water and reduction
 CC of nitrate and removal of nitrogen in waste water. The present sequence
 CC was used in the present invention.
 XX
 XX Sequence 1407 BP; 342 A; 341 C; 449 G; 275 T; 0 other;
 SQ

Query Match 84.5%; Score 1227.2; DB 22; Length 1407;
 Best Local Similarity 94.0%; Pred. No. 0;
 Matches 1319; Conservative 0; Mismatches 79; Indels 5; Gaps 4;

QY 4 TTGATCTGTGCTCAGAACGACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCGGAC 63
 DB 6 TTGATCATGCTCAGACAGCAGCCTGGCGCAGGCTTAACACATGCAAGTCGAGCGGCG 65
 QY 64 CTTGGGCTTACGCGCGGAGGTAGTAAACGGGTGGGACGCTGTCCTCTCTACGGAAT 123
 DB 66 CTTGGGCTTACGCGCGGAGGTAGTAAACGGGTGGGACGCTGTCCTCTCTACGGAAT 125
 QY 124 AGCCCGGGAACCTGGGAGTAACTACCGTATACGCTTTGGGGAAGATTATCGGAGA 193
 DB 126 AGTCTCGGGAACCTGGGAGTAACTACCGTATACGCTTTGGGGAAGATTATCGGAGA 195
 QY 184 AGGATCGGCGCGGTTGGATTAGTGTGGTGGTAACTGTCGCGCAGCGGATC 243
 DB 186 AGGATCGGCGCGGTTGGATTAGTGTGGTGGTAACTGTCGCGCAGCGGATC 245
 QY 244 CATAGTGTGTTGAGAGGATGATACGCCACACTGGGACTGAGACACGCGCCAGACTCCTA 303
 DB 246 CATAGTGTGTTGAGAGGATGATACGCCACACTGGGACTGAGACACGCGCCAGACTCCTA 305
 QY 304 CGGAGGACGACGCTGGGATCTTACACATAGGGGCAACCCCTGATCTAGCCATGCCGG 363
 DB 306 CGGAGGACGACGCTGGGATCTTACACATAGGGGCAACCCCTGATCTAGCCATGCCGG 365
 QY 364 TGAGTGTAGAGGCTTGGGTTGTAAGCTCTTTTCAGCTGGGGAAGATATGACGTAC 423
 DB 366 TGAGGATAGAGGCTTGGGTTGTAAGCTCTTTTCAGCTGGGGAAGATATGACGTAC 425
 QY 424 AGCAGAAGAGCCCGGCTAACTCCGTCGACGAGCGCGGTAACTACGGAGGGGGGTAGC 483
 DB 426 AGCAGAAGAGCCCGGCTAACTCCGTCGACGAGCGCGGTAACTACGGAGGGGGGTAGC 485
 QY 484 GTTGTTCGGGAATTACTTGGGGGTAAAGCGCAGCTAGCGGCACTGGAAAGTCAGAGGTGAAA 543

RESULT 12

AAC87598

ID AAC87598 standard; DNA; 1430 BP.

XX AAC87598;

XX AAC87598;

DT 16-MAR-2001 (first entry)

XX Bacterium SH134-8 (FERM P-17192) 16S rDNA.

DB 486 GTTGTTCGGAATTACTGGCGTTAAAGCGCACGTAGCGGATCAGAAAGTCAGAGGTGAAA 545
 QY 544 TCCAGGGCTCAACCTTGGAACTGCCCTTTTAAACTATCATCTGGAGTTCGAGAGAGGTG 603
 DB 546 TCCAGGGCTCAACCTTGGAACTGCCCTTTTAAACTCTGTGTGAGTTCGAGAGAGGTG 605
 QY 604 AGTGAATTCCGAGTGTAGAGTGAATTCGTAGATATTCGGAGGAACACACAGTGGCGAA 663
 DB 606 AGTGAATTCCGAGTGTAGAGTGAATTCGTAGATATTCGGAGGAACACACAGTGGCGAA 665
 QY 664 GCGGGCTCACTGGCTGATACCTGACCTGAGGTGCGAAAGCGTGGGAGCAACACAGATT 723
 DB 666 GCGGGCTCACTGGCTGATACCTGACCTGAGGTGCGAAAGCGTGGGAGCAACACAGATT 725
 QY 724 AGATACCTCTGATGTCACGCCCTTAACGATGAATCCAGACGTCGCGCAAGCATGCTGT 783
 DB 726 AGATACCTCTGATGTCACGCCCTTAACGATGAATCCAGACGTCGCGCAAGCATGCTGT 785
 QY 784 CGGTGTCACACCTAACCGGATTAAGCATTCGCCCTGGGAGTAGCGGTCCGAAGATTAAC 843
 DB 786 CGGTGTCACACCTAACCGGATTAAGCATTCGCCCTGGGAGTAGCGGTCCGAAGATTAAC 845
 QY 844 TCAAGGAATTGACGGGGGCGCCGACACAGCGGTGGAGCATGTGGTTTAATTCGAGCAAC 903
 DB 846 TCAAGGAATTGACGGGGGCGCCGACACAGCGGTGGAGCATGTGGTTTAATTCGAGCAAC 905
 QY 904 GCGCAAGAACCTTACCAACCTTGCACATGG-CAGGACCGCTGGAGAGATTCAGCTTTCTCG 962
 DB 906 GCGCAAGAACCTTACCAACCTTGCACATGGAGGAGGAGCGCTCCAGAGATGTTCTTTCTCG 965
 QY 963 TAAGAGA-CCTGTCACACAGGTGCTGCATGGCTGCTGTCAGCTCGTGTGAGATGTCG 1021
 DB 966 TAAGAGACCCCTCGCACAGGTGCTGCATGGCTGCTGTCAGCTCGTGTGAGATGTCG 1025
 QY 1022 GTTAAGTCGGGAACGAGCGCAACCGACGTCCTTAGTTGCCAGCAATTCAGTTGGGAAT 1081
 DB 1026 GTTAAGTCGGGAACGAGCGCAACCGACGTCCTTAGTTGGCAGC-ATTCAAGTTGGGCACT 1084
 QY 1082 CTATGAAACTGCGGATGATAAGTCGAGGAAGGTGGATGAGTCAAGTCCCTCATGGG 1141
 DB 1085 TTAGGAGAACTGCGGATGATAAGTCGAGGAAGGTGGATGAGTCAAGTCCCTCATGGG 1144
 QY 1142 CTTACGGGTGGGCTACACACGTCGTACAAATGGTGTGACAGTGGGTTAATCCCAAAA 1201
 DB 1145 CTTACGGGTGGGCTACACACGTCGTACAAATGGTGTGACAAATGGGCAATCCCAAAA 1204
 QY 1202 GCCATCTCAGTTCGGATTGCTCTGCAACTCGAGGCGATGAAGTTGGATCGGTAGTAA 1261
 DB 1205 GCCATCTCAGTTCGGATTGCTCTGCAACTCGAGGCGATGAAGTTGGATCGGTAGTAA 1264
 QY 1262 TCCGGAACAGCATGCGCGGTGAATACAGTTCCCGGCGCTTGTACACACCGCGCTGACA 1321
 DB 1265 TCCGGTACACGATGACGGGTGAATACAGTTCCCGGCGCTTGTACACACCGCGCTGACA 1324
 QY 1322 CCATGGAGTGTGTTTACCCGACGACGNTGCGCTAACCTTC--GGGGGCGAGCGGCCA 1379
 DB 1325 CCATGGAAATTGGTCTACCCGACGAGGTGCGCTAACCCGCAAGGGAGGCGCGGCCA 1384
 QY 1380 CGGTAGGATCAGCGACTGGGGTG 1402
 DB 1385 CGGTAGGCTCAGTGAAGTGGGGTG 1407

XX SH134-8; FERM P-17192; Gram negative; aerobic; heterotrophic;
 KW hydroxylaminodisulphonic acid; HADS decomposition; 16S rDNA; ds.
 XX Bacteria.
 OS JP2000287678-A.
 XX 17-OCT-2000.
 XX 09-APR-1999; 99JP-0102575.
 XX 09-APR-1999; 99JP-0102575.
 XX (MITO) MITSUBISHI JUKOYO KK.
 XX WPI; 2001-127271/14.
 DR A microbe decomposing a nitrogen-containing sulfur compound -
 XX Disclosure; Page 4; 5pp; Japanese.
 XX The invention relates to a novel bacterium, designated SH134-8 in
 CC the specification, which is able to decompose the nitrogen-containing
 CC sulphur compound HADS (hydroxylaminodisulfonic acid). Bacterium SH134-8
 CC (FERM P-17192) is an aerobic heterotrophic Gram-negative bacterium which
 CC is non-motile and has no sugar-assimilating ability. Bacterium SH134-8
 CC can be used for decomposing a nitrogen-containing sulphur compound such
 CC as HADS in a cost-effective manner e.g., for environmental
 CC decontamination. The present sequence represents DNA encoding 16S
 CC ribosomal RNA (16S rDNA) from bacterium SH134-8.
 XX Sequence 1430 BP; 342 A; 351 C; 456 G; 281 T; 0 other;
 SQ

Query Match 83.0%; Score 1205.4; DB 22; Length 1430;
 Best Local Similarity 92.1%; Pred. No. 0;
 Matches 1314; Conservative 0; Mismatches 107; Indels 5; Gaps 4;

QY 1 AGTTTGATCTGGCTCAGACGAACGCTGGGGCAGGCTTAACACATGCAAGTCGAGCGA 60
 DB 4 AGTTTGATCTGGCTCAGACGAACGCTGGGGCAGGCTTAACACATGCAAGTCGAGCGC 63
 QY 61 GACCTTCGGGTCTAGCGGCGACGGGTGAGTAACGCGTGGGAACGCTGCTCTACGG 120
 DB 64 GCCCTTCGGGTGAGCGGCGACGGGTGAGTAACGCGTGGGAACGCTGCTCTACGG 123
 QY 121 AATAGCCCCGGGAACCTGGGAGTAATACCGGTATACGCCCTTTGGGGAAAGATTATCGG 180
 DB 124 AATAGCCACTGGAAACGGTGAGTAATACCGCATACGCCCTTCGGGGGAAAGATTATCGG 183
 QY 181 AGAAGGATCGGCCCGCTTGGATTAGTAGTGTGGGTAAATGGCCACCAAGCCGACG 240
 DB 184 AGGAGGATCGGCCCGCTTGGATTAGTAGTGTGGGTAAATGGCCACCAAGCCGACG 243
 QY 241 ATCCATAdCTGGTTTGAAGGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTC 300
 DB 244 ATCCATAGCTGTTTGAAGGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTC 303
 QY 301 CTACGGGAGCAGCAGTGGGAAATCTTAGACAATGGGGCAACCCCTGATCTAGCCATGCC 360
 DB 304 CTACGGGAGCAGCAGTGGGAAATCTTAGACAATGGGGCAACCCCTGATCTAGCCATGCC 363
 QY 361 CGGTGAGTGAAGGCTTAGGTTTAAAGCTCTTTCAGCTGGGGAAGATAAATGACGGT 420
 DB 364 CGGTGAGTGAAGGCTTAGGTTTAAAGCTCTTTCAGCTGGGGAAGATAAATGACAGT 423
 QY 421 ACCAGCAGAGAAGCCCGGCTACTCGTCCAGCAGCCGCGGTAAATACGGGGGCGT 480
 DB 424 AGCAGGTAAGAAACCCCGGCTAACTCCGTCCAGCAGCCGCGGTAAATACGGGGGCGT 483
 QY 481 AGCGTTGTCGGAATTAAGTGGCGTAAAGCAGCAGTGGCGGACTGGAAAGTCAGAGTG 540
 DB 484 AGCGTTGTCGGAATTAAGTGGCGTAAAGCAGCAGTGGCGGACTGGAAAGTGGGGTG 543

QY 541 AAATCCAGGCTCAACCTTGAAGTCTGCTTTGAACTATCAGTCTGGAGTTCGAGAG 600
 DB 544 AAATCCAGGCTCAACCTTGAAGTCTGCTTTGAACTATCAGTCTGGAGTTCGAGAG 603
 QY 601 GTGAGTGAATTCGAGTGTAGAGTGAATTCGTAGATATTCGAGAGAACACCAAGTGC 660
 DB 604 GTGAGTGAATTCGAGTGTAGAGTGAATTCGTAGATATTCGAGAGAACACCAAGTGC 663
 QY 661 GAAGCGGCTCAGTGGCTGATAGTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 720
 DB 664 GAAGCGGCTCAGTGGCTGATAGTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 723
 QY 721 ATTAGATACCTCTGGTGTAGTCCACGCGTAAACGATGAATGCAGACGTCGGAAGCATGCT 780
 DB 724 ATTAGATACCTCTGGTGTAGTCCACACCGTAAACGATGAATGCAGACGTCGGAAGCATGCT 783
 QY 781 TGTGCTGTACACCTAACGATTAAGCATTCGCGCTGGGAGTACGCTCGCAAGATAA 840
 DB 784 TGTGCTGTACACCTAACGATTAAGCATTCGCGCTGGGAGTACGCTCGCAAGATAA 843
 QY 841 AACTCAAGGAATTCAGCGGCGCGCACAAAGCGTGGAGCATGTGTTTAAATTCGAAGC 900
 DB 844 AACTCAAGGAATTCAGCGGCGCGCACAAAGCGTGGAGCATGTGTTTAAATTCGAAGC 903
 QY 901 AACCGCGAGAACCTTACCACCTTTGACATGG-CAGGACCGCTGGAGAGATTTCAGCTTTC 959
 DB 904 AACCGCGAGAACCTTACCACCTTTGACATGGATATCGCGGACCGAGAGATTTCAGCTTTC 963
 QY 960 TCGTAAG-AGACCTGCACACAGTGTGCTCATGGTGTGCTGAGTGTGCTGAGATGT 1018
 DB 964 AGTTGCGGTGATATACACAGTGTGCTCATGGTGTGCTGAGTGTGCTGAGATGT 1023
 QY 1019 TCGTTTAAGTCCGCAAGGAGCGCAACCCAGCTCCCTAGTTGTCAGCAATTCGA-ATTTC 1077
 DB 1024 TCGTTTAAGTCCGCAAGGAGCGCAACCCAGCTCCCTAGTTGTCAGCAAGTTCGCTGG 1083
 QY 1078 AACTCTATGGAACCTGCGGATGAAGTGGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1137
 DB 1084 CACTCTGTGGAACCTGCGGATGAAGTGGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1143
 QY 1138 TGGCCCTTACGGGTGGGCTACACAGTGTGCTACATGTGTTGTTGAGTGTGTTTAAATCC 1197
 DB 1144 TGGCCCTTACGGGTGGGCTACACAGTGTGCTACATGTGTTGTTGAGTGTGTTTAAATCC 1203
 QY 1198 AAAAGCCATCTCAGTTCGGATTGCTCTGCAACTGCGAGGCGCATGAAGTGTGAATTCGCTA 1257
 DB 1204 AAAAGCCATCTCAGTTCGGATTGCTCTGCAACTGCGAGGCGCATGAAGTGTGAATTCGCTA 1263
 QY 1258 GTAATCGGGAACAGCATGCGCGTGAATACGTTCCCGGCGCTTGTACACACCGCCGCT 1317
 DB 1264 GTAATCGGGAACAGCATGCGCGTGAATACGTTCCCGGCGCTTGTACACACCGCCGCT 1323
 QY 1318 CACACCATGGAGTGTGTTTACCGGAGCGAGTGGCTGAAC--TTCCGGGGGAGCGG 1375
 DB 1324 CACACCATGGAGTGTGTTTACCGGAGCGCGTGGCTGAACCTTACCGGAGGAGCGG 1383
 QY 1376 GCCACGGTAGGATCAGCAGTGGGTTGAAGTGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1421
 DB 1384 ACCACGGTAGGCTCAGCAGTGGGTTGAAGTGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1429

RESULT 13

ABL40356

ID ABL40356 standard; DNA; 1430 BP.

XX ABL40356;

XX AC ABL40356;

XX DT 01-JUL-2002 (first entry)

XX DE Polynucleotide sequence specific to a HADS decomposing microbe.

XX KW HADS; decomposing; ds.

XX OS Roseobacter sp.
 XX PN JP2001346589-A.
 XX PD 18-DEC-2001.
 XX PF 08-JUN-2000; 2000JP-0172649.
 XX PR 08-JUN-2000; 2000JP-0172649.
 XX PA (MITO) MITSUBISHI JUROGYO KK.
 XX DR WPI; 2002-199320/26.
 XX PT Polynucleotide specific to a HADS decomposing microbe, and detection
 PT and determination of a HADS decomposing microbe using the
 PT polynucleotide.
 XX PS Claim 1; Page 7; 9pp; Japanese.
 XX CC The invention relates to a polynucleotide specific to a HADS decomposing
 CC microorganism, and detection and determination of a HADS decomposing
 CC microbe using the polynucleotides of the invention. Nucleotides of the
 CC invention are useful as probes or primers. The method is used for
 CC detecting or determining a HADS decomposing microbe. The current sequence
 CC represents a polynucleotide sequence specific to a HADS decomposing
 CC microbe.
 XX SQ Sequence 1430 BP; 342 A; 351 C; 456 G; 281 T; 0 other;
 Query Match 83.08; Score 1205.4; DB 24; Length 1430;
 Best Local Similarity 92.18; Pred. No. 0;
 Matches 1314; Conservative 0; Mismatches 107; Indels 5; Gaps 4;
 QY 1 AGTTGATCTCGTCTAGAACGAGCTGGCGGAGGCTTAACACATGCAAGTCGAGCGA 60
 DB 4 AGTTGATCTCGTCTAGAACGAGCTGGCGGAGGCTTAACACATGCAAGTCGAGCGC 63
 QY 61 GACCTCGGCTTAGCGGCGGAGGCTAGTACGCGTGGAACGTCGCCCTTCTACGG 120
 DB 64 GCCTTCGGGTGAGCGGCGGAGGCTAGTACGCGTGGAACGTCGCCCTTCTACGG 123
 QY 121 AATAGCCCGGGAACCTGAGTAATACCGTATACGCCCTTGGGGGAAGATTATCGG 180
 DB 124 AATAGCCACTTGAACCGGTGAGTAATACCGTATACGCCCTTGGGGGAAGATTATCGG 183
 QY 181 AGAAGGATCGGCCCGCTTGGATTAGTGTGGGTAAATGGCCCAACAGCCGACG 240
 DB 184 AGGAGGATCGGCCCGCTTGGATTAGTGTGGGTAAATGGCCCAACAGCCGACG 243
 QY 241 ATCCATAGCTGTTTGAAGGATGATCAGCCAGTGGGACTGAGACACGCGCCAGACTC 300
 DB 244 ATCCATAGCTGTTTGAAGGATGATCAGCCAGTGGGACTGAGACACGCGCCAGACTC 303
 QY 301 CTACGGGAGCAGCTGGGGAATCTTAGACATGGGGCAACCCCTGATCCCATGCC 360
 DB 304 CTACGGGAGCAGCTGGGGAATCTTAGACATGGGGCAACCCCTGATCCCATGCC 363
 QY 361 CGCTGAGTGTAGAGCGCTTAGGCTTGAAGCTCTTTCAGCTGGGAAGATATGACGGT 420
 DB 364 CGCTGAGTGTAGAGCGCTTAGGCTTGAAGCTCTTTCAGCTGGGAAGATATGACAGT 423
 QY 421 ACCAGCAGAAAGACCCCGCTAACTCCGTCGACGAGCGCGGTAAATACGGAGGGGCT 480
 DB 424 AGCAGGTAAAGAAACCCCGCTAACTCCGTCGACGAGCGCGGTAAATACGGAGGGGTT 483
 QY 481 AGCGTTGTCGGAATTAAGCGGTAAAGCGACAGTAGGCGGACTGGAAGTACAGAGTG 540
 DB 484 AGCGTTGTCGGAATTAAGCGGTAAAGCGACAGTAGGCGGACTGGAAGTACAGAGTG 543
 QY 541 AATCCAGGCTCAACCTTGGAACTGCCCTTTGAACTATCACTGAGCTCGAGTTCGAGAG 600

DB 544 AATCCGGGGCTCAACCCCGGAACCTGCCCTCCAAAACCTCTCAGTCTCGAGTTCGAGAG 603
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 QY 661 GAAGGGGCTCACTGGCTCGATACCTGACGCTGAGGTGCGAAAGCTGGGGAGCAAAACAGG 720
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 QY 721 ATTAGATACCTGTAGTCCACGCCCTTAAACGATGAATGCCAGACGTCGGCAAGCATGCT 780
 DB 724 ATTAGATACCTGTAGTCCACACCGTAAACGATGAATGCCAGTCTGCTCGGCAAGCATGCT 783
 QY 781 TGTCTGCTGTCACACCTTAACGGATTAAGCATTCGCCCTGGGGAGTACGGTTCGCAAGATTA 840
 DB 784 TGTCTGCTGTCACACCTTAACGGATTAAGCATTCGCCCTGGGGAGTACGGTTCGCAAGATTA 843
 QY 841 AACTCAAGGAATTTGACGGGGGCCGACAAAGCGGTGGAGCATGTGTTTAAATTCGAAGC 900
 DB 844 AACTCAAGGAATTTGACGGGGGCCGACAAAGCGGTGGAGCATGTGTTTAAATTCGAAGC 903
 QY 901 AAGCGCAGAACCTTACCAACCTTGCATGCG - CAGGACCGCTGGAGAGATTACGCTTTC 959
 DB 904 AAGCGCAGAACCTTACCAACCTTGCATGCG - CAGGACCGCTGGAGAGATTACGCTTTC 963
 QY 960 TCGTAG - AGACCTGTCACAGGTGCTGATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1018
 DB 964 AGTTCTGGCTGGATATCACAGGTGCTGATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1023
 QY 1019 TCGTTTAAGTCCGCGACGAGCGCAACCCAGTCCCTAGTTGCCAGCAATTC - GTTGGG 1077
 DB 1024 TCGTTTAAGTCCGCGACGAGCGCAACCCAGTCCCTAGTTGCCAGCAATTC - GTTGGG 1083
 QY 1078 AACTCTATGAAATCTGCCGATGATAAGTCGAGGAAGTGTGGATGACGTCAAGTCTCTCA 1137
 DB 1084 CACTCTGTGAAATCTGCCGATGATAAGTCGAGGAAGTGTGGATGACGTCAAGTCTCTCA 1143
 QY 1138 TGGGCTTACGGTGGCTTACACACGTGCTCAATGGTGTGATGACGTGGTTAATCCCT 1197
 DB 1144 TGGGCTTACGGTGGCTTACACACGTGCTCAATGGTGTGATGACGTGGTTAATCCCT 1203
 QY 1198 AAGAGCATCTCAGTTCGATGCTCTCACTGCACTGAGGCGCATGAAGTTCGAATCGCTA 1257
 DB 1204 AAGAGCATCTCAGTTCGATGCTCTCACTGCACTGAGGCGCATGAAGTTCGAATCGCTA 1263
 QY 1258 GATTCGCGAAGCAGCATGCGCGGTGAATACGTTCCCGGCGCTTGTACACACCGCCGT 1317
 DB 1264 GATTCGCGTAAACAGCATGACGCGGTGAATACGTTCCCGGCGCTTGTACACACCGCCGT 1323
 QY 1318 CACACATGGGAGTGTCTTACCCGACGAGGNTGCGCTAAC - TTCGGGGGCGACGGC 1375
 DB 1324 CACACATGGGAGTGTCTTACCCGACGCGCGTACCGCTTACCCCTTACCGGAGCGCG 1383
 QY 1376 GCCACGCTAGCATCAGCGACTGGGTGAAGTCGTAACAAGTAGCC 1421
 DB 1384 ACCACGCTAGCTCAGCGACTGGGTGAAGTCGTAACAAGTAGCC 1429
 RESULT 14
 ABL55947
 ID ABL55947 standard; DNA; 1484 BP.
 XX
 AC ABL55947;
 XX
 DT 14-JUN-2002 (first entry)
 XX
 DE Rhodobacter sphaeroides 16s rDNA SEQ ID NO 1.
 XX
 DE Rhodobacter; 16s rRNA; photosynthetic microbe; FERM P-18033;
 KW azo dye; decomposing; ds.
 XX
 OS Rhodobacter sphaeroides.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 09:18:53 ; Search time 111 seconds
(without alignments)
5773.769 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 1451 | 99.9 | 1452 | 1 | US-08-276-943-1 |
| 2 | 1451 | 99.9 | 1452 | 2 | US-08-716-841-1 |
| 3 | 1414.8 | 97.4 | 1430 | 2 | US-08-902-518A-1 |
| 4 | 1227.2 | 84.5 | 1407 | 4 | US-09-517-744B-1 |
| 5 | 1198.6 | 82.5 | 1419 | 4 | US-09-565-063-2 |
| 6 | 1086.4 | 74.8 | 1502 | 3 | US-09-187-946-2 |
| 7 | 1036.4 | 71.4 | 1415 | 2 | US-08-632-470-52 |
| 8 | 987.4 | 68.0 | 1556 | 3 | US-08-995-960-1 |
| 9 | 980.2 | 67.5 | 1508 | 2 | US-08-632-470-44 |
| 10 | 973.6 | 67.1 | 1436 | 4 | US-09-347-001-2 |
| 11 | 960.4 | 66.1 | 1438 | 4 | US-09-347-001-1 |
| 12 | 944.2 | 65.0 | 1494 | 2 | US-08-632-470-49 |
| 13 | 944 | 65.0 | 1440 | 2 | US-08-632-470-33 |
| 14 | 944 | 65.0 | 1440 | 2 | US-08-632-470-36 |
| 15 | 942.4 | 64.9 | 1440 | 2 | US-08-632-470-35 |
| 16 | 942 | 64.9 | 1438 | 2 | US-08-632-470-24 |
| 17 | 940.8 | 64.8 | 1440 | 2 | US-08-632-470-23 |
| 18 | 940.8 | 64.8 | 1440 | 2 | US-08-632-470-29 |
| 19 | 940.8 | 64.8 | 1458 | 2 | US-08-632-470-45 |
| 20 | 940 | 64.7 | 1436 | 2 | US-08-632-470-34 |
| 21 | 939.2 | 64.7 | 1440 | 2 | US-08-632-470-26 |
| 22 | 939.2 | 64.7 | 1440 | 2 | US-08-632-470-28 |
| 23 | 938.2 | 64.6 | 1441 | 2 | US-08-632-470-38 |
| 24 | 936 | 64.5 | 1440 | 2 | US-08-632-470-41 |
| 25 | 934.4 | 64.4 | 1440 | 2 | US-08-632-470-37 |
| 26 | 934.4 | 64.4 | 1440 | 2 | US-08-632-470-39 |
| 27 | 932.8 | 64.2 | 1440 | 2 | US-08-632-470-46 |

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|----|-------|------|------|---|------------------|-------------------|
| 28 | 932.4 | 64.2 | 1442 | 2 | US-08-632-470-30 | Sequence 30, Appl |
| 29 | 931.4 | 64.1 | 1439 | 2 | US-08-632-470-31 | Sequence 31, Appl |
| 30 | 931.2 | 64.1 | 1432 | 2 | US-08-632-470-25 | Sequence 25, Appl |
| 31 | 930 | 64.0 | 1569 | 2 | US-08-632-470-47 | Sequence 47, Appl |
| 32 | 929.6 | 64.0 | 1440 | 2 | US-08-632-470-43 | Sequence 43, Appl |
| 33 | 926.2 | 63.8 | 1427 | 2 | US-08-632-470-27 | Sequence 27, Appl |
| 34 | 920.4 | 63.4 | 1432 | 2 | US-08-632-470-32 | Sequence 32, Appl |
| 35 | 914.2 | 63.0 | 1498 | 2 | US-08-632-470-51 | Sequence 51, Appl |
| 36 | 913.8 | 62.9 | 1439 | 3 | US-08-632-470-42 | Sequence 42, Appl |
| 37 | 904.8 | 62.3 | 1208 | 3 | US-09-187-946-1 | Sequence 1, Appl |
| 38 | 904 | 62.3 | 1408 | 2 | US-08-632-470-40 | Sequence 40, Appl |
| 39 | 899.2 | 61.9 | 1483 | 3 | US-08-953-171-7 | Sequence 7, Appl |
| 40 | 863.8 | 59.5 | 1435 | 2 | US-08-632-470-48 | Sequence 48, Appl |
| 41 | 861.8 | 59.4 | 1501 | 4 | US-09-793-920A-1 | Sequence 1, Appl |
| 42 | 861.8 | 59.4 | 1501 | 4 | US-09-821-016-5 | Sequence 5, Appl |
| 43 | 861.8 | 59.4 | 1501 | 4 | US-09-745-416-1 | Sequence 1, Appl |
| 44 | 861.8 | 59.4 | 1501 | 4 | US-09-748-205-1 | Sequence 1, Appl |
| 45 | 857.6 | 59.1 | 1540 | 4 | US-09-228-184-1 | Sequence 1, Appl |

ALIGNMENTS

RESULT 1
US-08-276-943-1
; Sequence 1, Application US/08276943
; Patent No. 5607839
; GENERAL INFORMATION:
; APPLICANT: Tsukakura, Akira
; APPLICANT: Yoneda, Hisashi
; APPLICANT: Takaki, Mikihiro
; APPLICANT: Kiyota, Takashi
; TITLE OF INVENTION: BACTERIA BELONGING TO NEW GENUS AND
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF CAROTENOIDS USING SAME
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed & Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,943
; FILING DATE: 19-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MAKI, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 700085.407
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to rRNA
US-08-276-943-1

Query Match 99.9%; Score 1451; DB 1; Length 1452;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1452; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTTTGATCCTGGCTCAGAACGCTGCGGAGGCTTAACACATGCAAGTCGAGCGA 60

Db 1 AGTTTACCTGCTCAGAACGACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCGA 60
QY 61 GACCTTCGGGTCTAGCGCGGAGCGGTGAGTACCGGTGGGACGTCGCTTCTCTACGG 120
Db 61 GACCTTCGGGTCTAGCGCGGAGCGGTGAGTACCGGTGGGACGTCGCTTCTCTACGG 120
QY 121 AATAGCCCGGGAACCTGGGAGTAAATACCGTATACGCCCTTTGGGGGAAGATTTATCGG 180
Db 121 AATAGCCCGGGAACCTGGGAGTAAATACCGTATACGCCCTTTGGGGGAAGATTTATCGG 180
QY 181 AGAAGATCGCCCGGCTTGGATTAGTGTAGTGTGGGTAAATGGCCCAACCAAGCGGAG 240
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QY 241 ATCCATAGCTGTTTTCAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAGACTC 300
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QY 361 GCGTGAGTATGAAGCCCTTAGGTTGTAAGCTCTTTTCACTGGGGAAGATTAATGACGCT 420
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QY 421 ACCAGCAGAGAGCCCGGCTAACTCCGTGCCAGCAGCGCGGTAATACGAGGGGCT 480
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QY 481 AGCGTTGTTTCGGAATTAATCTGGCGTAAAGCGCACCTGAGCGGACTGGAAGTCAGAGTG 540
Db 481 AGCGTTGTTTCGGAATTAATCTGGCGTAAAGCGCACCTGAGCGGACTGGAAGTCAGAGTG 540
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Db 541 AAATCCAGGGCTAACCTTGAAGTGCCTTTGAACATCACTAGCTGGAGTTTCGAGAGAG 600
QY 601 GTGAGTGAATTCAGGCTGAGCTGAATTCGTAGATATTCGAGGAGNACACCACTGGC 660
Db 601 GTGAGTGAATTCAGGCTGAGCTGAATTCGTAGATATTCGAGGAGNACACCACTGGC 660
QY 661 GAAGCGGCTACTGGCTGATACGCTGAGCTGAGTGGGGAAGCGTGGGGAACCAACAGG 720
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QY 721 ATTAGATCCCTGTTAGTCCAGCGCTAAACGATGAATGCCAGAGCTGGCAAGCATGCT 780
Db 721 ATTAGATCCCTGTTAGTCCAGCGCTAAACGATGAATGCCAGAGCTGGCAAGCATGCT 780
QY 781 TGTGCGGTGTCACACCTAACGATTAAGCATTCGCGCTGGGAGTACGTCGCAAGATTAA 840
Db 781 TGTGCGGTGTCACACCTAACGATTAAGCATTCGCGCTGGGAGTACGTCGCAAGATTAA 840
QY 841 AACTCAAGGAATTCAGCGGGGCGCCGACAGCGGTGGAGCATGTGTTTAAATTCGAAGC 900
Db 841 AACTCAAGGAATTCAGCGGGGCGCCGACAGCGGTGGAGCATGTGTTTAAATTCGAAGC 900
QY 901 AACGGCGAGACCTTACCAACCTTGCATGCGAGGACCGCTGGAGAGATTACGCTTCT 960
Db 901 AACGGCGAGACCTTACCAACCTTGCATGCGAGGACCGCTGGAGAGATTACGCTTCT 960
QY 961 GGTAGAGACCTGTCACAGAGTGTGATGCGTGCCTGAGTGTGCTGAGATGTC 1020
Db 961 GGTAGAGACCTGTCACAGAGTGTGATGCGTGCCTGAGTGTGCTGAGATGTC 1020
QY 1021 GGTAAAGTCCGCAACGAGCGCAACCCAGCTCCCTAGTGTGCGACCAATTCAGTTGGGAAC 1080
Db 1021 GGTAAAGTCCGCAACGAGCGCAACCCAGCTCCCTAGTGTGCGACCAATTCAGTTGGGAAC 1080
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Db 1081 TCTATGGAATGCGGATGATAAGTCGGAGGAAGTGTGGATGACGTCAGCTCCTCATGG 1140
QY 1141 GCCTTACGGTGGGCTACACAGCTCTACATGGTGGTGCACAGTGGGTAAATCCCCAAA 1200
Db 1141 GCCTTACGGTGGGCTACACAGCTCTACATGGTGGTGCACAGTGGGTAAATCCCCAAA 1200
QY 1201 AGCCATCTCAGTTCGATTGCTCTGCAACTCGAGGGCATGAAGTTGGAATCGCTAGTA 1260
Db 1201 AGCCATCTCAGTTCGATTGCTCTGCAACTCGAGGGCATGAAGTTGGAATCGCTAGTA 1260
QY 1261 ATCGGGGAACAGATGCGCGGTGAATAGCTTCCCGGGCTGTACACACCGCGGCTC 1320
Db 1261 ATCGGGGAACAGATGCGCGGTGAATAGCTTCCCGGGCTGTACACACCGCGGCTC 1320
QY 1321 ACCATGGGAGTGGTCTTACCCGACGACGNTGGCTAACTTCGGGGGCGAGCGGCCAC 1380
Db 1321 ACCATGGGAGTGGTCTTACCCGACGACGNTGGCTAACTTCGGGGGCGAGCGGCCAC 1380
QY 1381 GGTAGATCAGGACTGGGGTGAAGTCGTAACAAAGTAGCGGTAGGGGAACCTTCGGGCTG 1440
Db 1381 GGTAGATCAGGACTGGGGTGAAGTCGTAACAAAGTAGCGGTAGGGGAACCTTCGGGCTG 1440
QY 1441 GATCACCCTCTT 1452
Db 1441 GATCACCCTCTT 1452

RESULT 2

US-08-716-841-1
; Sequence 1, Application US/08716841
; Patent No. 5858761
; GENERAL INFORMATION:
; APPLICANT: Tsubokura, Akira
; APPLICANT: Yoneda, Hisashi
; APPLICANT: Takaki, Mikihiro
; APPLICANT: Kiyota, Takashi
; TITLE OF INVENTION: BACTERIA BELONGING TO NEW GENUS AND
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF CAROTENOIDS USING SAME
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed & Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,841
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,943
; FILING DATE: 19-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 700085,407
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to rRNA

US-08-716-841-1

| Query Match | | 99%* | Score 1451; | DB 2; | Length 1452; | |
|-----------------------|-----|--|---------------|-----------|--------------|--|
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| Matches 1452; | | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; | |
| QY | 1 | AGTTGATCTGCTCAGAACGAGCGTGGCGGAGGCTTAACACATCGAAGTCCAGCGA | 60 | | | |
| DB | 1 | AGTTGATCTGCTCAGAACGAGCGTGGCGGAGGCTTAACACATCGAAGTCCAGCGA | 60 | | | |
| QY | 61 | GACCTTCGGGCTCAGCGGAGCGGCTGAGTAACGCGTGGGAAAGTCCCTCTCTACGG | 120 | | | |
| DB | 61 | GACCTTCGGGCTCAGCGGAGCGGCTGAGTAACGCGTGGGAAAGTCCCTCTCTACGG | 120 | | | |
| QY | 121 | AATAGCCCCGGAACTCGGAGTAAATACCGTATACGCGCTTTGGGGGAAAGATTATCGG | 180 | | | |
| DB | 121 | AATAGCCCCGGAACTCGGAGTAAATACCGTATACGCGCTTTGGGGGAAAGATTATCGG | 180 | | | |
| QY | 181 | AGAGGATCGCCCGCTGATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT | 240 | | | |
| DB | 181 | AGAGGATCGCCCGCTGATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT | 240 | | | |
| QY | 241 | ATCATAGCTGCTTGGAGGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTC | 300 | | | |
| DB | 241 | ATCATAGCTGCTTGGAGGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTC | 300 | | | |
| QY | 301 | CTACGGGAGGAGCGAGTGGGAATCTTAGACAATGGGGGCAACCTGATCTAGCCATGCC | 360 | | | |
| DB | 301 | CTACGGGAGGAGCGAGTGGGAATCTTAGACAATGGGGGCAACCTGATCTAGCCATGCC | 360 | | | |
| QY | 361 | CGTGAGTATGAGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG | 420 | | | |
| DB | 361 | CGTGAGTATGAGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGG | 420 | | | |
| QY | 421 | ACCAGCAGAGAGCGCGCTACTCGCTCCAGCAGCGCGCTAAATACGAGGGGCT | 480 | | | |
| DB | 421 | ACCAGCAGAGAGCGCGCTACTCGCTCCAGCAGCGCGCTAAATACGAGGGGCT | 480 | | | |
| QY | 481 | AGCGTGTTCGGAATTAAGCGGCTAAAGCGCAGCTAGCGGAGCTGGAAGTTCAGAGTG | 540 | | | |
| DB | 481 | AGCGTGTTCGGAATTAAGCGGCTAAAGCGCAGCTAGCGGAGCTGGAAGTTCAGAGTG | 540 | | | |
| QY | 541 | AAATCCAGGCTCAACCTTGGAGTCTTGAACATATAGTCTGAGTTCGAGAGAG | 600 | | | |
| DB | 541 | AAATCCAGGCTCAACCTTGGAGTCTTGAACATATAGTCTGAGTTCGAGAGAG | 600 | | | |
| QY | 601 | GTGAGTGAATTCGAGTATAGAGTGAATTCGAGTATTCGAGGAGACACAGTGGC | 660 | | | |
| DB | 601 | GTGAGTGAATTCGAGTATAGAGTGAATTCGAGTATTCGAGGAGACACAGTGGC | 660 | | | |
| QY | 661 | GAAGCGGCTCAGTGGCTGATACGCTGAGTGGGAGGAGCGTGGGAGCAACAGG | 720 | | | |
| DB | 661 | GAAGCGGCTCAGTGGCTGATACGCTGAGTGGGAGGAGCGTGGGAGCAACAGG | 720 | | | |
| QY | 721 | ATTAGATACCTGTGATCCAGCGCTAAAGCATGAATGCGAGAGTCCGGAAGCATGCT | 780 | | | |
| DB | 721 | ATTAGATACCTGTGATCCAGCGCTAAAGCATGAATGCGAGAGTCCGGAAGCATGCT | 780 | | | |
| QY | 781 | TGTCGGTTCACACCTACGATTAAGCATTCGCGCTGGGAGTACGCTCGCAAGTAA | 840 | | | |
| DB | 781 | TGTCGGTTCACACCTACGATTAAGCATTCGCGCTGGGAGTACGCTCGCAAGTAA | 840 | | | |
| QY | 841 | AACCTAAAGGATTAAGCGGCGCCGACAGCGTGGAGCATGTGTTTAAATCGAAGC | 900 | | | |
| DB | 841 | AACCTAAAGGATTAAGCGGCGCCGACAGCGTGGAGCATGTGTTTAAATCGAAGC | 900 | | | |
| QY | 901 | AACGGCAGAACCTTACCAACCTTACATGCGAGAGCGCTGGAGAGATTTCAGTTCT | 960 | | | |
| DB | 901 | AACGGCAGAACCTTACCAACCTTACATGCGAGAGCGCTGGAGAGATTTCAGTTCT | 960 | | | |
| QY | 961 | CGTAAGACACCTGACAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 1020 | | | |
| DB | 961 | CGTAAGACACCTGACAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 1020 | | | |

| | | | |
|----|------|---|------|
| QY | 1021 | GGTTAAGTCCGGCAGACGAGCGAACCACCGTCCCTAGTTCGCCAGCAATTCAGTTGGGAC | 1080 |
| DB | 1021 | GGTTAAGTCCGGCAGACGAGCGAACCACCGTCCCTAGTTCGCCAGCAATTCAGTTGGGAC | 1080 |
| QY | 1081 | TCTATGGAACCTGCCGATGATAAGTCGGAGGAAGTGTGGATGACGTCAAGTCCCTCATGG | 1140 |
| DB | 1081 | TCTATGGAACCTGCCGATGATAAGTCGGAGGAAGTGTGGATGACGTCAAGTCCCTCATGG | 1140 |
| QY | 1141 | GCCTTACGGGTTGGGCTACACACGTCGTACATATGTTGGTGTGAGTGGGTTAATCCCCAAA | 1200 |
| DB | 1141 | GCCTTACGGGTTGGGCTACACACGTCGTACATATGTTGGTGTGAGTGGGTTAATCCCCAAA | 1200 |
| QY | 1201 | AGCATCTCAGTTCGGATTCCTCTGCAACTCGAGGCGATGAAGTTGGAATCGCTAGTA | 1260 |
| DB | 1201 | AGCATCTCAGTTCGGATTCCTCTGCAACTCGAGGCGATGAAGTTGGAATCGCTAGTA | 1260 |
| QY | 1261 | ATCGGGGAACAGCAGTCCGCGTGAATACGTTCCCGGGCTTGTACACACCGCCCGTAC | 1320 |
| DB | 1261 | ATCGGGGAACAGCAGTCCGCGTGAATACGTTCCCGGGCTTGTACACACCGCCCGTAC | 1320 |
| QY | 1321 | ACCATGGAGTTCGTTCTACCGGACGAGTTCGCTAACCTTCGGGGGCGAGCGGCCAC | 1380 |
| DB | 1321 | ACCATGGAGTTCGTTCTACCGGACGAGTTCGCTAACCTTCGGGGGCGAGCGGCCAC | 1380 |
| QY | 1381 | GGTAGATCAGGAGTGGGTTGAAGTCTGTAAAGTGTAGTCCGAGGAGAACCTCGGGCTG | 1440 |
| DB | 1381 | GGTAGATCAGGAGTGGGTTGAAGTCTGTAAAGTGTAGTCCGAGGAGAACCTCGGGCTG | 1440 |
| QY | 1441 | GATCACCCTTCCT 1452 | |
| DB | 1441 | GATCACCCTTCCT 1452 | |

RESULT 3

US-08-902-518A-1
Sequence 1, Application US/08902518A
Patent No. 5935808

GENERAL INFORMATION:

APPLICANT: Joseph Hirschberg and Mark Harker
TITLE OF INVENTION: NOVEL CAROTENOID-PRODUCING BACTERIAL
TITLE OF INVENTION: SPECIES AND PROCESS FOR PRODUCTION
TITLE OF INVENTION: OF CAROTENOIDS USING SAME
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark M. Friedman c/o Robert Sheinbein
STREET: 2940 Birchtree Lane
CITY: Silver Spring
STATE: Maryland
COUNTRY: United States of America
ZIP: 20906

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted to
SOFTWARE: an ASCII file

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/902,518A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Friedman, Mark M.

REGISTRATION NUMBER: 33,883

REFERENCE/DOCKET NUMBER: 325/20

TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-5625553

| | | |
|------|--|------|
| 421 | GGCTAACTCGTGCCACAGCCGCGGTAAATACGGAGGGGGCTAGCGGTTATTTCGGAAATAC | 480 |
| 499 | TGGCGCTAAAGCCAGCAGCTAGCGGACTGGAAGACTCAGAGGTGAAATCCCAAGGCTCAACC | 558 |
| 481 | TGGCGCTAAAGCCAGCAGCTAGCGGACTGGAAGTCAAGGTGAAATCCCGGGGCTCAACC | 540 |
| 559 | TTGGAACTGCGTTTGAACCTATCAGTCTCGAGTTCGAGAGAGGTGAGTGGAAATCCCGAGT | 618 |
| 541 | CCGGAACTGCGTTTGAACCTCCAGCTCTTAGGTTCGAGAGAGGTGAGTGGAAATCCCGAGT | 600 |
| 619 | GTAGAGGTGAAATTCGTAGATATTCGGAGGAAACACAGTGGCGAAGGCGGCTCACTGGCT | 678 |
| 601 | GTAGAGGTGAAATTCGTAGATATTCGGAGGAAACACAGTGGCGAAGGCGGCTCACTGGCT | 660 |
| 679 | CGATACTGACGCTGAGGTGCGAAAGCGTGGGAGCAACAGAGATTAGATACCTTGGTAGT | 738 |
| 661 | CGATACTGACGCTGAGGTGCGAAAGCGTGGGAGCAACAGAGATTAGATACCTTGGTAGT | 720 |
| 739 | CCAGCGCGTAACGATGAATGCCAGACGTCGGCAAGCATGCTTGTTCGGTGTCAACACTAA | 798 |
| 721 | CCAGCGCGTAACGATGAATGCCAGTCGTCGGCGACATGCTGTTCCGTTGACACACTAA | 780 |
| 799 | CGGATTAAAGCATTCGCCCTGGGGAGTACGGTCGCAAGATTAAACCTCAAGGAATTCAGC | 858 |
| 781 | CGGATTAAAGCATTCGCCCTGGGGAGTACGGTCGCAAGATTAAACCTCAAGGAATTCAGC | 840 |
| 859 | GGGGCCCGCACAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGACAACCTTACC | 918 |
| 841 | GGGGCCCGCACAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGACAACCTTACC | 900 |
| 919 | AACCTTTGACATGGC-AGGACCGCTGGAGAGATTACGTTTCTCGTGAAG-AGACCTTCAC | 976 |
| 901 | AACCTTTGACATGGCCATCGCGTTCCAGAGATGGTTCTTTCAGTTTCGGCTGGATCGCAC | 960 |
| 977 | ACAGGTGCTGATGGCTGCTGCAGCTCGTGCAGATGTTTCGGTTAAGTCCGCGAAC | 1036 |
| 961 | ACAGGTGCTGATGGCTGCTGCAGCTCGTGCAGATGTTTCGGTTAAGTCCGCGAAC | 1020 |
| 1037 | GAGCGAACCCACGTCCTCAGTTGCCAGCAATTCAGTTGGGAACCTATATGGAACCTGCG | 1096 |
| 1021 | GAGCGAACCCACGTCCTCAGTTGCCAGC-ATTTCAGTTGGGCACCTTCGGGAACTGCG | 1079 |
| 1097 | ATGATTAAGTCGGAGGAAGGTGTGGATGAGTCAAGTCTCTATGCGGCTTACGGGTTGGGC | 1156 |
| 1080 | GTGATTAAGTCGGAGGAAGGTGTGGATGAGTCAAGTCTCTATGCGGCTTACGGGTTGGGC | 1139 |
| 1157 | TACACAGCTGTACATAATGGTGTGACAGTGGGTTAATCCCAAAGCCCATCTCAGTTCCG | 1216 |
| 1140 | TACACAGCTGTACATAATGGCAGTGACANTGGGTTAATCCCAAAGCTGTCTCAGTTCCG | 1199 |
| 1217 | ATTGTCTCTGCAACTCGAGGGCATGAAGTTGGAATCGCTAGTAATTCGGGGAACAGCATG | 1276 |
| 1200 | ATTGGGCTGTCAACTCGACCCCATGAAGTCGGAATCGCTAGTAATTCGCGTAACAGCATG | 1259 |
| 1277 | CCGCGGTGAATACGTTCCCGGGCTTGTACACACCCCGCTACACACCATTCGGAGTTGGTT | 1336 |
| 1260 | ACCGGTGAATACGTTCCCGGGCTTGTACACACCCCGCTACACACCATTCGGAGTTGGTT | 1319 |
| 1337 | CTACCCGAGGACGNTTCGGTAACTTCTGCGGAGGAGGCGAGCCAGCATAGGATCAGT | 1379 |
| 1320 | CTACCCGAGGCGTTCGCCCACTCGCAGAGAGGAGGCGAGCCAGCATAGGATCAGT | 1379 |
| 1393 | GACTGGGGTGAAGTCTGATAAAGGTAGCCGTAGGGGAACC | 1432 |
| 1380 | GACTGGGGTGAAGTCTGATAAAGGTAGCCGTAGGGGAACC | 1419 |

RESULT 6

RESOL 8
US-09-187-946-2/c

Sequence 2, Application US/09187946

; Patent No. 6255467

; GENERAL INFORMATION:

APPLICANT: Lindner, Luther E.

Db 722 GCTTTGAGCATCCGCTGGGAGTACGTCGCAAGATTAAACTCAAAGGAATGACGG 663
QY 860 GGGCCCGCACAGCGGTGAGCATGTTTAAATCGAAGCAACGGCAGAACCTTACCA 919
Db 662 GGGCCCGCACAGCGGTGAGCATGTTTAAATCGAAGCAACGGCAGAACCTTACCA 603
QY 920 ACCCTTGACATGCGCAGGACCGCTGGAGAGATTCAGCTTCTCGTAAGACACCTGCACACA 979
Db 602 TCCCTTGACATGCGCTGTATCCACAGAGATTGGGTCCACTTCGGTGGCCGCACACA 543
QY 980 GGTGCTGATGCTGCTGACGCTGCTGCGAGATGTTGCGTTAAAGTCCGGCAGACAG 1039
Db 542 GGTGCTGATGCTGCTGACGCTGCTGCGAGATGTTGCGTTAAAGTCCGGCAGACAG 483
QY 1040 CGCAACCCACGCTCCCTAGTCCACCAATTCAGTTGGGACACTCTATGGAACCTGCCGATG 1099
Db 482 CGCAACCCACGCTCCCTAGTCCATC - ATTCAAGTTGGGACACTCTAGGAGACTGCCGGTG 424
QY 1100 ATAAAGTCG - GAGGAAGGTGTGATGACGCTCAAGTCTCTATGGGCTTACGGGTTGGGCTA 1158
Db 423 ATAAAGTCG - GAGGAAGGTGTGATGACGCTCAAGTCTCTATGGGCTTACGGGTTGGGCTA 364
QY 1159 CACAGCTGCTCAATGTTGGTGAACAGTGG - -----GTTAATCCCC 1197
Db 363 CACAGCTGCTCAATGTTGGTGAACAGTGG - -----GTTAATCCCC 304
QY 1198 AAAGCCATCTCAGTTGCGATGCTCTGCAACTCGAGGCGATGAAGTTGGAATCGGTA 1257
Db 303 AAAGCCATCTCAGTTGCGATGCTCTGCAACTCGAGTGCATGAAGCGGGAATCGGTA 244
QY 1258 GTAATCGGGACACAGCTCCGCGGTGAATAGTTCCCGGGCTGTACACACCCGCGT 1317
Db 243 GTAATCGGGACACAGCTCCGCGGTGAATAGTTCCCGGGCTGTACACACCCGCGT 184
QY 1318 CACACCATGAGGAGTTGTTTACCGGACGAGTGCCTAAGTTCGCGGGGCGCAGCGCGC 1377
Db 183 CACACCATGAGGAGTTGTTTACCGGACGAGTGCCTAAGTTCGCGGGGCGCAGCGCGC 124
QY 1378 CACGCTAGATCAGGACTGGGTTGAAGTCGTAACAGGTAGCCGTAGGGGAACTGGG 1437
Db 123 CACGCTAGGTCAGGACTGGGTTGAAGTCGTAACAGGTAGCCGTAGGGGAACTGGG 64
QY 1438 CTGGA 1442
Db 63 CTGGA 59

RESULT 7

US-08-632-470-52
; Sequence 52, Application US/08632470
; Patent No 5976791
; GENERAL INFORMATION:
; APPLICANT: MABILAT, CLAUDE
; TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF
; TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RNA AND
; TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE
; STREET: P.O. BOX 19928
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/632,470

; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BERRIDGE, WILLIAM P
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38238
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)-836-6400
; TELEFAX: (703)-836-2787
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1415 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-632-470-52

Query Match 71.4%; Score 1036.4; DB 2; Length 1415;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 1230; Conservative 0; Mismatches 157; Indels 30; Gaps 7;
QY 14 CTCAGAACGACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCG - AGACCTTCGGGTC 72
Db 1 CTCAGAACGACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCGCACTCTTTTAGAGT 60
QY 73 TAGCGCGGACGCGGTGAGTAACGCTGGGAAAGTCCCTTCTACGGAATAGCCCCGGG 132
Db 61 GAGCGGCAAAACGCGGTGAGTAACGCTGGGAAATCTACCCATCTCTACGGAATACACAGAG 120
QY 133 AAACGTGGGAGTAATACCGTATACG - CCGTTTGGGGAAAGATTATTCGAGAGGATCGG 191
Db 121 AAATTTGTGCTAATACCGTATACGTCCTCTGGGAGAAAGATTATTCGAGAGGATGAG 180
QY 192 CCGCGTTGGATTAGTGTAGTGTGGGTAAATGGCCCAACCAACGACGATCCATAGCTG 251
Db 181 CCGCGTTGGATTAGTGTAGTGTGGGTAAAGGCTCACCAGGCGACGATCCATAGCTG 240
QY 252 GTTTCAGAGGATGATCAGCCACACACACACACACACACACACACACACACACACACAC 311
Db 241 GTCTGAGAGGATGATCAGCCACACACACACACACACACACACACACACACACACACAC 300
QY 312 AGCAGTGGGGAATCTTAGACAATGGGGCAACCCCTGATCTAGCATGCGCGGTGAGTGAT 371
Db 301 AGCAGTGGGGAATCTTAGACAATGGGGCAACCCCTGATCTAGCATGCGCGGTGAGTGAT 360
QY 372 GAAGCCCTTAGGGTTGTTAAAGCTCTTTCAGCTGGGAAGATAATAGCGTACCAGCAGAAG 431
Db 361 GAAGCCCTTAGGGTTGTTAAAGCTCTTTCAGCGGTGAAGATAATAGCGTTAACCGGAGAAG 420
QY 432 AAGCCCGGCTAACCTTCGTCGACGCGCGGTAAATACGAAAGGGGGGTAGCGTTGTTCCG 491
Db 421 AAGCCCGGCTAACCTTCGTCGACGCGCGGTAAATACGAAAGGGGGGTAGCGTTGTTCCG 480
QY 492 GAATTACTGGCGTAAAGCGCACGACGACGACGACGACGACGACGACGACGACGACGACG 551
Db 481 GATTACTGGCGTAAAGCGCATGATGAGCGGATATTAAGTCAGAGGTGAATATCCAGGG 540
QY 552 CTCACCTTGGAACTGCCCTTTGAAACTATCATCTGAGTCTGAGTCTCGAGAGAGGTGAGTGAAT 611
Db 541 CTCACCTTGGAACTGCCCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 612 TCCGAGTGTAGAGGTGAATTCGCTAGATATTCGAGAGGAACACCACTGCGGAAGGGCGCTC 671
Db 601 TCCGAGTGTAGAGGTGAATTCGCTAGATATTCGAGAGGAACACCACTGCGGAAGGGCGCTC 660
QY 672 ACTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 731
Db 661 ACTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 732 TGGTAGTCCAGCCGCTAAACGATGAATGATGATGATGATGATGATGATGATGATGATGATGAT 791
Db 721 TGGTAGTCCAGCCGCTAAACGATGAATGATGATGATGATGATGATGATGATGATGATGATGAT 780

APPLICATION NUMBER: US/08/995,960
FILING DATE: 22-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, David S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 1826/47986
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1556 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: rRNA
US-08-995-960-1

Query Match 68.0%; Score 987.4; DB 3; Length 1556;
Best Local Similarity 83.7%; Pred. No. 0;
Matches 1210; Conservative 0; Mismatches 207; Indels 29; Gaps 7;

QY 1 AGTTGATCTGCTCAGAACGAGCGTGGCGGCGAGCTTAACACATGCAAGTCGAGCGA 60
DB 112 AGTTGATCTGCTCAGAACGAGCGTGGCGGCGAGCTTAACACATGCAAGTCGAGCGA 171
QY 61 GACCTCGGCTGCTAGCGCGGCGAGCGTGAAGCGGTGGGAGCGTCCCTCTCTACGG 120
DB 172 GATCTCGGATCTAGTGGCGGCGAGCGTGAAGCGGTGGGAGCGTCCCTCTCTACGG 231
QY 121 AATGACCGCGGAGAACTGGGAGTAATACCGTATACCGCTTTGGGGGAAAGATTATCGG 180
DB 232 AATAACAGTTGGAAACGACGTCTAATACCGGATGATGACGTAAGTCCAAAGATTATCGC 291
QY 181 AGAAGGATCGCGCGCGCTGGATTAGTGTGGGTAAATGGCCCAACCGCGAGC 240
DB 292 CAGAGGATGAGCGCGCGCTAGGATTAGTGTGGGTAAAGAGCGCAGCGAGC 351
QY 241 ATCCATAGCTGTTGAGAGGATGATCAGGCACACTGGGACTGAGACGCGCCAGAGTC 300
DB 352 ATCCTTAGCTGGTCTGAGAGGATGATCAGGCACACTGGGACTGAGACGCGCCAGAGTC 411
QY 301 CTACGGGAGGCGAGCTGGGGAATCTTAGACAATGGGGGCAACCTGATCTAGCATGCC 360
DB 412 CTACGGGAGGCGAGCTGGGGAATCTTAGACAATGGGGGCAACCTGATCTAGCATGCC 471
QY 361 CGGTGAG-TGATGAGCGCTTAGGTTGTAAGCTCTTTCAGCTGGGAA-CATATGAGC 418
DB 472 CGGTGAGTTGATGAAAGCCTTAGGTTGTAAGCTCTTTCAGCTGGGAA-CATATGAGC 531
QY 419 GTACCGACAGAAAGCGCGCTAACCTCCGTCGACGAGCGCGGTAATACGAGGCGG 478
DB 532 GTACCGGAGGATGAGCTCCGCTAACCTCCGTCGACGAGCGCGGTAATACGAGGAG 591
QY 479 CTACCGTGTTCGGAATTAATCTGGCGTAAACCGCACGCTAGGCGGACTGGAAGTCAGAGG 538
DB 592 CTACCGTGTTCGGAATTAATCTGGCGTAAACCGCACGCTAGGCGGCTTTGTAAGTTAGAGG 651
QY 539 TGAATCCGAGGCTCAACCTTGGAACTGCGCTTGAACACTATCATCTGAGTTCGAGTTCGAGAG 598
DB 652 TGAAGGCTGGAGCTCAACTCCAGAAATGCGCTTAAAGACTCATCTGCTTGAATCCAGGAG 711
QY 599 AGGTGAGTGAATCCGAGTGTAGAGGTGAATTCGTAGATATTCGGAGGAGCAACAGCTG 658
DB 712 AGGTGAGTGAATTCGGAGTGTAGAGGTGAATTCGTAGATATTCGGAGGAGCAACAGCTG 771
QY 659 GCGAAGGCGGCTCACTGGCTGATACCTGAGGTGCGAAAGCGTGGGAGCGCAACA 718

792 CACCTAACGATTAAAGCATTCGCGCTGGGAGTACGTCGCAAGATTAAACCTCAAGGA 851
DB 781 CAGCTACGCGTTAAACATTCGCCCTGGGAGTACGTCGCAAGATTAAACCTCAAGGA 840
QY 852 ATTGACGGGGCGCCGACAGCGGTGGAGCATGTGTTTAAATTCGAAGCAACGCGCAGAA 911
DB 841 ATTGACGGGGCGCCGACAGCG-GTGAGCATGTGTTTAAATTCGAAGCAACGCGCAGAA 899
QY 912 CTTTACCAACCTTGATCGGAGGAGCGGTGGAGGATTCAGCTTCTCGTAAAGAGACC 971
DB 900 CTTTACCAACCTTGATCGGAGGAGCGGTGGAGGATTCAGCTTCTCGTAAAGAGACC 959
QY 972 TGCAC---ACAGGTGCTGATCGTCTGCTGAGTCTGCTGAGATCTTCGGTTAAG 1027
DB 960 GGATCGGTGATCGTCTGCTGAGTCTGCTGAGTCTTCGGTTAAG 1019
QY 1028 TCCGGCAACGAGGCGCAACCGCTCCCTAGTTGCCAGCAATTCAGTTGGGAACTCTATGG 1087
DB 1020 TCCGGCAACGAGGCGCAACCGCTCCCTAGTTGCCATC-ATTAAGTTGGGCACTCTAGGG 1078
QY 1088 AACTGCCGATGATAGTCG-GAGGAAGGTGTGATGACGTCAAGTCTCATGGCGCTTA 1146
DB 1079 GGACTGCGGTGATAGCCGAGAGGAGGTGGGATGACGTCAAGTCTCATGGCGCTTA 1138
QY 1147 CGGTGCGGTACACAGCTGCTCAATGTTGGTGGACAGTGG----- 1187
DB 1139 CGGCTGGGTACACAGCTGCTCAATGTTGGTGGACAGTGGGCGAGCGAGCCGCGAGGTC 1198
QY 1188 --GTTAATCCCAAAAGCCATCTCAGTTGCGGATGTCTCTGCAACTCGAGGCGATGAAG 1245
DB 1199 GAGCTAATCTCCAAAGCCATCTCAGTTGCGGATTCGCAACTCGAGTGCAGTGAAG 1258
QY 1246 TTGGAATCGTGTAGTAATCGCGGAGACAGCATGCGCGGTGTAATAGTTCCCGGGCTTGTA 1305
DB 1259 TTGGAATCGTGTAGTAATCGTGGATCAGCATGCCAGGTGAATAGTTCCCGGGCTTGTA 1318
QY 1306 CACACCGCGGTACACCATGCGGAGTGGTCTACCGGAGCGAGTCCGCTACCTTCGG 1365
DB 1319 CACACCGCGGTACACCATGCGGAGTGGTCTACCGGAGCGAGTCCGCTACCTTCGG 1378
QY 1366 GGGGAGCGCGCCAGGCTAGGATCAGCGACTGGGGTG 1402
DB 1379 GAGGAGCGCAACCGATGAGGTCAGCGACTGGGGTG 1415

RESULT 8
US-08-995-960-1
Sequence 1, Application US/08995960
Patent No. 6030818
GENERAL INFORMATION:
APPLICANT: FAGI, Michel
APPLICANT: LANDRY, Nathalie
APPLICANT: BOISSINOT, Maurice
APPLICANT: HILIE, Marie-Claude
APPLICANT: HARVEY, Mario
APPLICANT: GAGNI, Martin
TITLE OF INVENTION: BACTERIAL MASS PRODUCTION
TITLE OF INVENTION: OF TAXANES AND PACLITAXEL
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:

Db 772 CGAAGCGGCTACTGACCTGGTATTGACGCTGAGGTGCGAAGCGTGGGAGCAACA 831
Qy 719 GGATTAGATACCTGTGTAGTCCAGCGCTTAACGATGAATGCCAGACGTCGCAAGCATG 778
Db 832 GGATTAGATACCTGTGTAGTCCAGCGCTTAACGATGAATGCCAGACGTCGCAAGCATG 891
Qy 779 CT-TGTGCTGTACACCTAAGGATTAAGCATTCCTGCTGGGAGTACGCTCGCAAGAT 837
Db 892 GTCTTTGGTGGCGAGCTACGATTAAGTATTCCTGCTGGGAGTACGCGCCGCAAGGT 951
Qy 898 TAAACTCAAAAGGAATGACGGGGCCGCAACGCGTGGAGCATGTGGTTAATTGGA 897
Db 952 TAAACTCAAAAGGAATGACGGGGCCGCAACGCGTGGAGCATGTGGTTAATTGGA 1011
Qy 898 AGCAACGCGGAGAACCTTACCAACCTTTGACATGCGCAGGACGCGT--GGAGAGATTCAGC 955
Db 1012 AGCAACGCGGAGAACCTTACCAACCTTTGACATGCGCAGGATTCCTGGAGACAGATCT 1071
Qy 956 TTTCTCGTAAGAGACCTGCACACAGGTGCTGCATGGCTGTGTCAGCTCGTCTGTGAGA 1015
Db 1072 CTTCCTTCGGGAGCTGGAACGCGAGTGTGCTGATGGCTGTGTCAGCTCGTCTGTGAGA 1131
Qy 1016 TGTTCGTTAAGTCCGCAAGCAGGCGCAACCCAGCTCCCTAGTTCGCCAGCAATTCAGTTG 1075
Db 1132 TGTTCGTTAAGTCCGCAAGCAGGCGCAACCCAGCTCCCTAGTTCGCCAGCAATTCAGTTG 1190
Qy 1076 GGAATCTATGGAATCCGATGATGAATGATGCGGAGGAGGTGTGATGACGTCAGTCAAGTCT 1135
Db 1191 GGGACTCTAAAGGAACCCGCGTGTATGAACGCGGAGGAGGTGGGATGACGTCAGTCAAGTCT 1250
Qy 1136 CATGGCCTTACGCTGGGCTACACAGCTGCTCAATGTTGGTGACAGTGG----- 1187
Db 1251 CATGGCCTTACGCTGGGCTACACAGCTGCTCAATGTTGGTGACAGTGG----- 1310
Qy 1188 -----GTTAATCCCAAAAGCCATCTCAGTTCGGATGTCTCTGCAACTCG 1234
Db 1311 CTCGGAGAGTGCCTATCTCCAAAGCGCTCAGTTCGGATGTCTCTGCAACTCG 1370
Qy 1235 AGGCATGAATGGAATCGTAGTAATCGGCGGACACGATGCGCGGTGTAATCGTTCC 1294
Db 1371 AGGCATGAAGCGGGAATCGTAGTAATCGGCGGACACGATGCGCGGTGTAATCGTTCC 1430
Qy 1295 CGGCGCTGTACACACCGCGTACACACGATGCGGAGTGTCTACCGCAGCAGCAGTCCG 1354
Db 1431 CAGGCGTGTACACACCGCGTACACACGATGCGGAGTGTCTACCGCAGCAGCAGTCCG 1490
Qy 1355 CTAACCTTCGCGGGGCGGCGGCGGAGGATGAGTACGCGACTGGGCTGAAGTCTTAAC 1412
Db 1491 CTAACCTGTAGAGAGGAGGCGGCGGAGGATGAGTACGCGACTGGGCTGAAGTCTTAAC 1550
Qy 1413 AAGGTA 1418
Db 1551 AAGGTA 1556

RESULT 9

US-08-632-470-44

; Sequence 44, Application US/08632470

; Patent No. 5976791

; GENERAL INFORMATION:

; APPLICANT: MABILAT, CLAUDE

; APPLICANT: RAOUT, DIDIER

; TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF

; TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND

; TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OLIFF & BERRIDGE

; STREET: P.O. BOX 19928

; CITY: ALEXANDRIA

; STATE: VA

; COUNTRY: USA

; ZIP: 22320

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,470
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38238
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-836-6400
TELEFAX: (703)-836-2787
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1508 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-632-470-44

Query Match 67.5%; Score 980.2; DB 2; Length 1508;

Best Local Similarity 81.8%; Pred. No. 0;

Matches 1220; Conservative 0; Mismatches 229; Indels 43; Gaps 6;

Qy 1 AGTTTGATCTCGCTCAGAACGAGCTGGCGGAGGCTTAACACATGCAAGTCGAGCGA 60
Db 19 AGTTTGATCTCGCTCAGAACGAGCTATCGGTATGCTTAACATGCAAGTCGAGCGG 78
Qy 61 GACCTTCGGGTCTAGC-----GGCGACGCGGTGAGTAACGCGTGGGTAATGCG 106
Db 79 ATTAAGTACGAGCTCGCTTTAGTTAATTAGTGGCAGACGCGGTGAGTAACGCGTGG 138
Qy 107 GCGCTTCCTACGGAATAGCCCCGGGAACTGGGAGTAATACGTAATACGCGCTTTGGG 166
Db 139 ACCCATCATGAGGAACTACTTTTAAATAAAGCTAATACCGTATATCTCTACGGAG 198
Qy 167 GAAAGATTATCGGAGAGGATCGCCCGCTTGGATTAGGTAGTGTGGGTAAATGCG 226
Db 199 GAAAGATTATCGCTGATGGATGGCGCCGCTCAGATTAGGTAGTGTGGGTAAATGCG 258
Qy 227 CCACCAAGCCGACGATCCATAGCTGTTTGAGAGGATGATCAGCCACACTGGGACTG 286
Db 259 TCACCAAGCCGACGATCTGTAGCTGTCTGAGAGGATGATCAGCCACACTGGGACTG 318
Qy 287 CAGGCGCCAGACTCTACGCGGAGGAGCAGTGGGGAATCTTAGACAATGGGCGCAACCT 346
Db 319 CAGGCGCCAGACTCTACGCGGAGGAGCAGTGGGGAATCTTAGACAATGGGCGCAACCT 378
Qy 347 GATCTAGCAGCTCGCGGTGAGTGAAGGCTTAGGCTTGAAGCTCTTTTCAGCTGGG 406
Db 379 GATCAGCAATACCGAGTGAAGGCTTAGGCTTGAAGCTCTTTTCAGCTGGG 438
Qy 407 AAGATAATGACGCTACCGAGCAAGAACCCCGGCTTAACCTCCGTCAGCAGCAGCGGTA 466
Db 439 AAGATAATGACGCTTACTTGCAGAAAAAGCCCGGCTTAACCTCCGTCAGCAGCAGCGGTA 498
Qy 467 ATACGAGGCGCTAGCGTTTTCGGAATTAATCTGGGCTTAAGAGGAGTGGGCGGACTG 526
Db 499 AGACGAGGCGGCTAGCGTTTTCGGAATTAATCTGGGCTTAAGAGGAGTGGGCGGCTTA 558
Qy 527 GAACTCAGAGTGAATCCCAAGGCTCAACCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 586
Db 559 GAACTTGAAGTGAAGGCGGCGCTTAACCTCGAATGTCTTCAAAACACTACTAATCT 618
Qy 587 GGAGTTCGAGAGAGGTGAGTGAATTCGAGGTGATAGAGGTGAATTCGATAGATTCGGA 646
Db 619 AGAGTGTAGTAGGGATGATGGAATTCCTAGTGTAGAGGTGAATTCCTAGATATAGGA 678

Db 781 TTCAAGTGTGGAAGTAACTGTTAAGCACACCGCTGGGAGTACGACCGCAAGTTGAA 840
QY 842 ACTCAAGGAATTACGGGGGCGGCACACGCGTGGAGATGTTGTTAAATCGAAGCA 901
Db 841 ACTCAAGGAATTACGGGGGCGGCACACGCGTGGAGATGTTGTTAAATCGAAGCA 900
QY 902 ACGGCGAAGCTTACCAACCTTGACATGCGCAGGACCGCTGGAGAGATTACAGCTTCTC 961
Db 901 ACGGCGAAGCTTACCAAGTCTGTTATGGGAGGACGCTGTCAGAGATGATATTC-- 958
QY 962 GTAAGAGACCTGCACACAGGTGCTGCATGGCTGCTGTCAGCTGCTGTCGAGATGTTTCG 1021
Db 959 -TTCGGACCTCCCGCACAGGTGCTGCATGGCTGCTGTCAGCTGCTGTCGAGATGTTGG 1017
QY 1022 GTTAAGTCCGCAACGAGCGCAACCCAGCTCCCTAGTTGCCAGCA-ATTCAAGTTGGGAAC 1080
Db 1018 GTTAAGTCCGCAACGAGCGCAACCCCTGCTTTAGTTGCCATCAGTTTGGGTGGGCAC 1077
QY 1081 TCTATGGAACCTGCGGATGATAAGTCCGAGGAAGGTGTTGATGAGTCAAGTCCCTCATGG 1140
Db 1078 TCTAGAGAGACTGCGGTGACACGCGGAGAGAGTGGGATGAGTCAAGTCCCTCATGG 1137
QY 1141 GCCTTACGGGTGGGCTACACACGTCTACATGTTGTTGTCAGTGG----- 1187
Db 1138 CCTTATGACCTGGGCTACACAGGTGCTACATGTCGCAATGGGAAGCTACATGTT 1197
QY 1188 -----GTTAATCCCAAGGACCTCAGTTCGGATGTTGCTCTGCACTCGAGGCG 1239
Db 1198 GACATGATGCGGATCTCAAAAACCGTCTCAGTTCGGATTGCACTCTGCACTCGAGTGC 1257
QY 1240 ATGAAGTTGGAATGCTAGTAAATCGCGGACAGCATGCGCGGTGAATACGTTCCCGGCG 1299
Db 1258 ATGAAGTTGGAATGCTAGTAAATCGCGGACAGCATGCGCGGTGAATACGTTCCCGGCG 1317
QY 1300 CTGTTACACACCGCGCTCACACCATGGGAGTTGTTCTACCCGACGACGNTGCGCTAAC 1359
Db 1318 CTGTTACACACCGCGCTCACACCATGGGAGTTGTTGACCTTAAAGCGGTGAGCGAAC 1377
QY 1360 CTTCGGGGGAGGCGGCGCAGGTAGGATCAGCGACTGGGTTGAAGTGTACACAAGTTA 1418
Db 1378 CGAAGGCGCAGCGACCCCGGTGCGGTCAGCGACTGGGTTGAAGTGTACACAAGTTA 1436

RESULT 11

US-09-347-001-1

; Sequence 1, Application US/09347001A

; Patent No. 6335177

; GENERAL INFORMATION:

; APPLICANT: MIHARA, Yasuhiro

; APPLICANT: TAKEUCHI, Sonoko

; APPLICANT: JOJIMA, Yasuko

; APPLICANT: TONOUCHI, Naoto

; APPLICANT: FUDOU, Ryoosuke

; APPLICANT: YOKOZEKI, Kenzo

; TITLE OF INVENTION: NOVEL MICROORGANISM AND METHOD FOR PRODUCING XYLITOL OR

; TITLE OF INVENTION: D-XYLULOSE

; FILE REFERENCE: 0010-1015-0

; CURRENT APPLICATION NUMBER: US/09/347,001A

; CURRENT FILING DATE: 1999-07-02

; EARLIER APPLICATION NUMBER: JP 10-193472

; EARLIER FILING DATE: 1998-07-08

; EARLIER APPLICATION NUMBER: JP 10-310398

; EARLIER FILING DATE: 1998-10-30

; EARLIER APPLICATION NUMBER: JP 11-12244

; EARLIER FILING DATE: 1999-01-20

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1438

; TYPE: DNA

; ORGANISM: Unknown Organism

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: strain P528

; FEATURE:

; OTHER INFORMATION: N at position 1365 is A, T, G, or C

US-09-347-001-1

Query Match

Best Local Similarity 66.1%; Score 960.4; DB 4; Length 1438;

Matches 1183; Conservative 82.3%; Pred. No. 6.1e-315;

Indels 27; Gaps 6;

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Db 1 TGATCCTGCTCAGAACCAACGCTGGCGCAGCGCTTTACACATGCAAGTCGAGCGAGACC 60

QY 65 TTCGGGTCTAGCGCGGAGGTAGTAAACGCGTGGAGACGTCCTCTCTACGGAATA 124

Db 61 TTCGGGTCTAGCGCGGAGGTAGTAAACGCGTGGAGATCTATCCACGGGTGGGGGATA 120

QY 125 GCCCGGGAAACTGGGAGTAAATACCGTATACGCCCTTTGGGGGAAAG--ATTATTCGGAG 182

Db 121 ACACGTGGAAACTGGTGTCTAATACCGCATGATACCTGAGGGTCAAAGGCGCGAGTCGCCT 180

QY 183 AAGGATCGCCCGCTTGGATTAGGTAGTGGTGGGTAAATGCCCAACCAAGCCGACGAT 242

Db 181 GTGGAGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

QY 243 CCATAGCTGTTGAGAGGATGATCAGCCACACTGGGACTGGAGACGCGCCAGACTCCT 302

Db 241 CCATAGCTGTTGAGAGGATGATCAGCCACACTGGGACTGGAGACGCGCCAGACTCCT 300

QY 303 ACGGAGGCGAGCTGGGGAATCTTAGACAATGGGGCAACCTGATCTAGCATGCCGC 362

Db 301 ACGGAGGCGAGCTGGGGAATCTTAGACAATGGGGCAACCTGATCTAGCATGCCGC 360

QY 363 GTGAGTGTAAAGGCTTTAGGTTGTAAAGCTCTTTTACGTGGGAAGATAATGACGGTAC 422

Db 361 GTGTGTGAAGAGGCTTTCGGATTGTAAAGCACTTTTCGACGGGAGCATGATGACGGTAC 420

QY 423 CAGCAGAAAGCCCGCTTAACCTCGTCCAGCAGCGCGGTAAATACGAGGGGGCTAG 482

Db 421 CCGTAGAAGAACCCCGCTTAACCTCGTCCAGCAGCGCGGTAAATACGAGGGGGCTAG 480

QY 483 CCGTTGTCGGAATTAATCTGGGCGTAAAGCGACGCTAGCGGACTGGAAAGTCAGAGGTGAA 542

Db 481 CCGTTGTCGGAATTAATCTGGGCGTAAAGCGGCTGTTGTTACACTGAGTGTGAA 540

QY 543 ATCCAGGCTCAACCTTGGAACTGCTTTGAACTATCAGTCTGAGGTTCAGAGAGGT 602

Db 541 ATCCAGGCTTAACTTGGGCTGCTTTGATATACGTAGCTAGAGTGTGAGAGAGG 600

QY 603 GAGTGAATTCGAGTGTAGAGTGAATTCGATATTCGAGGAACACCAAGTCGCGA 662

Db 601 TTGTGAATTCGAGTGTAGAGTGAATTCGATATTCGAGGAACACCAAGTCGCGA 660

QY 663 AGCGGCTCAGTGGCTCGATCTAGCTGAGGTGCGAAAGGCTGGGAGCAACAGGAT 722

Db 661 AGCGGCAACCTGGCTCATGCTAGCTGAGCGCGGCGGAAAGCTGGGAGCAACAGGAT 720

QY 723 TAGATACCTGCTAGTCTCAGCGCTTAAACGATGAATGCCAGAGCTGCGCAAGCATCTTG 782

Db 721 TAGATACCTGCTAGTCTCAGCGCTTAAACGATGAATGCCAGAGCTGCGCAAGCATCTTG 780

QY 783 -TCGGTGTACACCTTAAACGATTAAGCATTCGCTGGGAGTACGCTGCGAGATTAA 841

Db 781 CTCAGTGTGAAGCTAAACGCTAAGCACACCGCTTGGGAATGACGCGCAAGGTTGAA 840

QY 842 ACTCAAGGAATTGACGGGGCGGCACACGCGGTGGAGCATGTTGTTTAAATCGAAGCA 901

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QY 902 ACGCGCAGAACCTTACCAACCTTGACAT-GGCAGGACCGCTGGAGAGATTCAGCTTTCT 960

Db 901 ACGCGCAGAACCTTACCAACCTTGACATGGGAGGCTGTACTCAGAGATGGGTATTTC 960

Db 960 CTTCTTACAGAGGCGCAGTTCGGCTGGGCTGCACAGGTGCTGCTATGCTGTC 1019
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Db 1020 AGCTGGTGCCTGATGTTTCGGTTAAGTCCGGCACAGCGCAACCCACGCTCCCTAGTT 1079
QY 1060 GCCAGCAATTCATGTTGGAACTCTATGGAACCTGCGATGATTAAGTCCGGAGGAGGTG 1118
Db 1080 ACCAGCGGTATGCGGCGCACTTTAAGGAACCTGCCATGATTAAGTCCGGAGGAGGTG 1139
QY 1119 GGAATGACGTCATGCTATGCGGCTTACGGTTCGGCTTACACAGCTGCTACAATGGTGG 1178
Db 1140 GGAATGACGTCATGCTATGCGGCTTACGGTTCGGCTTACACAGCTGCTACAATGGTGG 1199
QY 1179 TGCACATGGGT-----TAATCCCAAAAGCCATCTCAGTTCCGA 1217
Db 1200 CTACATAGTTGTCACAGCTGCGAAGGCTGAGCTAATCCGTAAGTTCAGTTCCGA 1259
QY 1218 TTGTCCTCTGCAACTCGAGGCGATGAAGTTGGAATCGCTAGTAATCGCGAAGCAGCATGC 1277
Db 1260 TTGTCCTCTGCAACTCGAGGCGATGAAGTTGGAATCGCTAGTAATCGCGAAGCAGCATGC 1319
QY 1278 CCGGTGGAATAGTTCCTGCGGCTTGTACACACCGCCGCTACACAGCTGGAGTTGGTTC 1337
Db 1320 CACGGTGAATAGTTCCTGCGGCTTGTACACACCGCCGCTACACAGCTGGAGTTGGCTT 1379
QY 1338 TACCCGACACGNTGCGCTAACCTTCGGGGGCGAGCGGCCAGCTAGATCAGCCACTG 1397
Db 1380 AACTCGAAGCTGTCGCGCAACCGTAAGGAGCGACCATTTAAGTTGGTTCGGTCACTG 1439
QY 1398 GGGTGAAGTCGTAACAGGTAGCGGTAGGGGAACCTGCGGCTGGATCACTCCTT 1452
Db 1440 GGGTGAAGTCGTAACAGGTAGCTGTAGTGAACCTGCGGCTGGATCACTCCTT 1494

RESULT 13
US-08-632-470-33
; Sequence 33, Application US/08632470
; Patent No. 5976791
; GENERAL INFORMATION:
; APPLICANT: RAOULT, CLAUDE
; APPLICANT: RAOULT, DIDIER
; TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF
; TITLE OF INVENTION: HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RNA AND
; TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE
; STREET: P.O. BOX 19928
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/632,470
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BERRIDGE, WILLIAM P
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38238
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)-836-6400
; TELEFAX: (703)-836-2787
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1440 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-632-470-33
Query Match 65.0%; Score 944; DB 2; Length 1440;
Best Local Similarity 81.7%; Pred. No. 2.3e-309;
Matches 1179; Conservative 0; Mismatches 221; Indels 43; Gaps 6;
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Db 1 CTTGGCTCAGAACGCTGGCGGAGGCTTAAACACATGCAAGTTCGAGGAGACCTTCG 60
QY 69 GGTCTAGC-----GGCGGACGGGTGAGTAAACGCTGGGAACGTCCTCTCT 114
Db 61 GGGCTTCTCTAATTTAGTTAGTGGCAGACGGGTGAGTAAACGCTGGGAATCTACCATCA 120
QY 115 CTACGGAATAGCCCGGAACTGGGAGTAATACCGTATACGCGCTTTGGGGGAAAGATT 174
Db 121 GTACGGAATAGCTTTTGAATAAAGCTAATACCGTATATCTCTACGAGGAAAGATT 180
QY 175 TATCGGAGAGGATCGCGCGCTTGGATTAGTATGTTGGTGGGTAATGCGCCACCAAG 234
Db 181 TATCGTGTATGATGATGACCGCGCTCAGATTAGTATGTTGGTGGGTAATGCGTCAACG 240
QY 235 CCGACGATCCATAGCTGGTTTGAAGAGTATCAGCCACACTGGGACTGAGACACGCGCC 294
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QY 295 AGACTCCTACGGGAGGACGAGTGGGGAATCTTACGCAATGGGGCAACCTCTGATCTAGC 354
Db 301 AGACTCCTACGGGAGGACGAGTGGGGAATTTGGCAATGGCGAAAGCTTATCCAGC 360
QY 355 CATCGCGGTAGTATGATGAAGGCTTAGGGTTGTAAAGCTCTTTTACGCTGGGAAGATAAT 414
Db 361 AATACCGAGTGTATGATGAAGGCTTAGGGTTGTAAAGCTCTTTTACGCAAGGAATAAT 420
QY 415 GACGCTACACAGCAGAGAGACCGCGGCTACTCGTCCGACAGCGCGGTATACGGAG 474
Db 421 GACGCTACTTGCAGAAAAGCGCGGCTAACTCCGTCGACAGCGCGGTATAGCGAG 480
QY 475 GGGCTAGCGTCTTGGGAATTAAGCGCTAAAGCGCAGTGGGCGACTGGAAGCTCA 534
Db 481 GGGCTAGCGTCTTGGGAATTAAGCGCTAAAGCGCAGTGGGCGGTATAGTATAGTTG 540
QY 535 GAGGTGAAATCCACAGGCTCAACCTTTGGAATCCCTTTGAAACTATCAGTCTGGAGTTCG 594
Db 541 GAAGTGAAGCGCGGCTTAACCTCGGAATTCCTTCAAAACTACTAATCTAGAGTGA 600
QY 595 AGAGAGGTGATGGAATTCGAGTGTAGAGTGAATTCGATATATTCGAGGAGACACC 654
Db 601 GTAGGGGATGATGGAATTCCTAGTGTAGAGTGAATTCCTAGTATATAGGAGACACC 660
QY 655 AGTGGGAGGCGGCTCAGTGGCTGATGCTGAGTGTAGGTCGGAAGCGTGGGAGCA 714
Db 661 GGTGGGAGGCGGCTCAGTGGCTGATGCTGAGTGTAGGTCGGAAGCGTGGGAGCA 720
QY 715 AACAGATTAGATACCTTGGTGTAGTCCACGCGTAAACGATGAATGCCAGCTCGGCAAG 774
Db 721 AACAGATTAGATACCTTGGTGTAGTCCACGCGTAAACGATGAATGCCAGCTCGGCAAG 779
QY 775 CATGCTTGGGTGTACACCTAACGGATTAAAGCTTCCCGCTGGGGAGTACGGTTCGCA 834
Db 780 ATTCTCTTTCGGTTTCGACGTAACGCTAACGCTTCCCGCTGGGGAGTACGGTTCGCA 839
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Db 900 CGATGTTACCGGAAAACCTTACCAACCTTACATGCGTGGTCCCGGATCGCAGATGC 959

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OM nucleic - nucleic search, using sw model

Run on: July 28, 2003, 10:53:33 ; Search time 356 Seconds
(without alignments)
8414.261 Million cell updates/sec

Title: US-10-049-228-1

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_RA:*

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- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1380 | 95.0 | 1426 | 14 | US-10-049-228-2 |
| 3 | 1093.6 | 75.3 | 1466 | 9 | US-09-726-774-12 |
| 4 | 1086.4 | 74.8 | 1502 | 10 | US-09-894-467-2 |
| 5 | 1044.6 | 71.9 | 1490 | 9 | US-09-900-876-2 |
| 6 | 973.6 | 67.1 | 1436 | 9 | US-09-902-693-2 |
| 7 | 960.4 | 66.1 | 1438 | 9 | US-09-902-693-1 |
| 8 | 904.8 | 62.3 | 1208 | 10 | US-09-894-467-1 |
| 9 | 881.4 | 60.9 | 105184 | 11 | US-09-847-513A-1 |
| 10 | 869.8 | 59.7 | 1532 | 13 | US-10-007-725-6 |
| 11 | 863.4 | 59.5 | 1494 | 13 | US-10-007-725-5 |
| 12 | 861.8 | 59.4 | 1501 | 9 | US-09-791-592-1 |
| 13 | 861.8 | 59.4 | 1501 | 9 | US-09-745-476-1 |
| 14 | 861.8 | 59.4 | 1501 | 9 | US-09-821-016-5 |
| 15 | 861.8 | 59.4 | 1501 | 9 | US-09-748-205-1 |
| 16 | 861.8 | 59.4 | 1501 | 9 | US-09-793-920A-1 |

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|------|-------|------|---------|----|--------------------|
| 17 | 861.8 | 59.4 | 1501 | 10 | US-09-951-720-1 |
| 18 | 861.8 | 59.4 | 1501 | 11 | US-09-791-610-1 |
| 19 | 861.8 | 59.4 | 1501 | 14 | US-10-218-519-5 |
| 20 | 861.8 | 59.4 | 1501 | 14 | US-10-266-787-5 |
| 21 | 861.8 | 59.4 | 1501 | 14 | US-10-252-518-5 |
| 22 | 861.8 | 59.4 | 1501 | 14 | US-10-105-305-1 |
| 23 | 861.8 | 59.4 | 1501 | 14 | US-10-133-404A-1 |
| 24 | 857.6 | 59.1 | 1540 | 10 | US-09-967-376-1 |
| 25 | 857.6 | 59.1 | 1540 | 14 | US-10-260-647-1 |
| 26 | 848.8 | 58.5 | 1481 | 9 | US-09-737-297-4 |
| 27 | 841 | 57.9 | 1467 | 9 | US-09-726-774-3 |
| 28 | 840.4 | 57.9 | 1541 | 9 | US-09-027-439-7 |
| 29 | 839.4 | 57.8 | 1542 | 11 | US-09-940-925A-158 |
| 30 | 839.4 | 57.8 | 1542 | 11 | US-09-941-925A-158 |
| 31 | 839.4 | 57.8 | 1542 | 14 | US-10-061-071-33 |
| 32 | 830.8 | 57.2 | 1541 | 9 | US-09-726-774-2 |
| 33 | 830 | 57.2 | 1549 | 9 | US-09-913-020-89 |
| 34 | 830 | 57.2 | 1549 | 9 | US-09-913-020-242 |
| 35 | 830 | 57.2 | 1549 | 9 | US-09-912-020-402 |
| 36 | 819.4 | 56.4 | 1544 | 9 | US-09-726-774-5 |
| 37 | 815.4 | 56.2 | 1553 | 10 | US-09-974-300-4446 |
| 38 | 814.2 | 56.1 | 1500 | 9 | US-09-726-774-4 |
| 39 | 813.8 | 56.0 | 1552 | 10 | US-09-974-300-8479 |
| 40 | 812.8 | 56.0 | 1830121 | 14 | US-10-329-960-1 |
| c 41 | 812.8 | 56.0 | 1830121 | 14 | US-10-329-960-1 |
| 42 | 809.8 | 55.8 | 1506 | 9 | US-09-027-439-3 |
| 43 | 809.2 | 55.7 | 1424 | 14 | US-10-007-527A-12 |
| 44 | 809.2 | 55.7 | 1424 | 14 | US-10-007-452-12 |
| c 45 | 806 | 55.5 | 7455 | 14 | US-10-219-227-19 |

ALIGNMENTS

RESULT 1

US-10-049-228-1
; Sequence 1, Application US/10049228
; Publication No. US2003004486A1
; GENERAL INFORMATION:
; APPLICANT: TSUBOKURA, Akira
; APPLICANT: MIYATA, Haruyoshi
; TITLE OF INVENTION: PROCESS OF PRODUCING CAROTENOID PIGMENTS
; FILE REFERENCE: 38331-0003
; CURRENT APPLICATION NUMBER: US/10/049,228
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: PCT/JP01/04874
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: JP 2000-175124
; PRIOR FILING DATE: 2000-06-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence corresponding to the 16S ribosomal RNA o

| | | | |
|----|----|--|-----|
| QY | 1 | AGTTTGATCTCGGCTCAGAACGAGCTGGCGGAGGCTTACACATGCAAGTCGAGCGA | 60 |
| DB | 1 | AGTTTGATCTCGGCTCAGAACGAGCTGGCGGAGGCTTACACATGCAAGTCGAGCGA | 60 |
| QY | 61 | GACCTTCGGGCTAGCGGCGGACGGTGTAGTAACTGGGACCTGCGCTCTCTACGG | 120 |

Db 61 GACCTTGGGCTTACGGCGGACGGGTGAGTAACCGTGGGAACGTGCCCTTCTCTACGG 120
Qy 121 AATAGCCCGGGAACATGGGAGTAAATACCGTATACGCCCTTTGGGGGAAGATTATTCGG 180
Db 121 AATAGCCCGGGAACATGGGAGTAAATACCGTATACGCCCTTTGGGGGAAGATTATTCGG 180
Qy 181 AGAAGGATCGCCCGCGTGGATTAGGTAGGTAGTGTGGGGTAATGCCCCACCAACCGGACG 240
Db 181 AGAAGGATCGCCCGCGTGGATTAGGTAGGTAGTGTGGGGTAATGCCCCACCAACCGGACG 240
Qy 241 ATCCATAGCTGGTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGCCCCAGACTC 300
Db 241 ATCCATAGCTGGTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGCCCCAGACTC 300
Qy 301 CTACGGAGGACAGTGGGAATCTTAGACAATGGGGCAACCTGATCTAGCCATGCC 360
Db 301 CTACGGAGGACAGTGGGGAATCTTAGACAATGGGGCAACCTGATCTAGCCATGCC 360
Qy 361 GCGTGAAGTGAAGGCTTAGGGTTGTAAGCTCTTTACGCTGGGAAGATAATGACGGT 420
Db 361 GCGTGAAGTGAAGGCTTAGGGTTGTAAGCTCTTTACGCTGGGAAGATAATGACGGT 420
Qy 421 ACCAGCAGAAAGCCCGGCTAACTCGTCCAGCAGCCCGGTATACGGAGGGGCT 480
Db 421 ACCAGCAGAAAGCCCGGCTAACTCGTCCAGCAGCCCGGTATACGGAGGGGCT 480
Qy 481 AGCGTTGTCGAATTAAGTGGCGTAAAGCCAGTAGGCGGACTGGAAGTCAAGAGTG 540
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Qy 541 AAATCCAGGCTCAACCTTGAAGTGGCTTTGAACTATCAGTCTGGAGTTCAGAGAG 600
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Qy 601 GTGAGTGAATTCGAGTGTAGAGGTGAATTCGTAGATATTCGGAGAACACCAAGTGGC 660
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Qy 661 GAAGCGCTCAGTGGCTGATGAGTGGCTGAGTGGTGGAGCGGAGGAGCAACAGG 720
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Qy 721 ATTAGATACCTGGTGTACCGCGGTAACGATGAATGCCAGACGTCGGCAACATGCT 780
Db 721 ATTAGATACCTGGTGTACCGCGGTAACGATGAATGCCAGACGTCGGCAACATGCT 780
Qy 781 TGTGGTGTACACCTAACGGATTAAGCATTCGCCCTGGGGAGTACGGTCCCAAGATTAA 840
Db 781 TGTGGTGTACACCTAACGGATTAAGCATTCGCCCTGGGGAGTACGGTCCCAAGATTAA 840
Qy 841 AACTCAAGGAATTCAGGGGCGCCGACAGCGGTGGAGCATCTGGTTTAATTCGAGC 900
Db 841 AACTCAAGGAATTCAGGGGCGCCGACAGCGGTGGAGCATCTGGTTTAATTCGAGC 900
Qy 901 AACCGCGTAACCTTACCAACCTTGATGATGGCAGGACCGCTGGAGAGATTACGCTTCT 960
Db 901 AACCGCGTAACCTTACCAACCTTGATGATGGCAGGACCGCTGGAGAGATTACGCTTCT 960
Qy 961 CGTAAGAGACCTGCACACAGTGTGATGGCTGTGATGGCTGTGATGGTGTGATGGTTC 1020
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Qy 1021 GGTAAAGTCCGGCAACGAGCGCAACCCAGTCCCTAGTTCGACCAATTCAGTTGGGAC 1080
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Db 1081 TCTATGAAATCGCGGATGATAAGTTCGGAGGAAGTGTGATGACGTCAGTCTCATGG 1140
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Db 1141 GCCTTAGGGTGGCTTACACACGCTGTGATCAATGGTGGTACAGTGGGTAAATCCCAAA 1200

Qy 1201 AGCCATCTCAGTTCGGATTGCTCTCAACTCGAGGGCATGAAGTTGGAATCGTAGTA 1260
Db 1201 AGCCATCTCAGTTCGGATTGCTCTCAACTCGAGGGCATGAAGTTGGAATCGTAGTA 1260
Qy 1261 ATCCGGAAACAGCATGCCGGTGAATACGTTCCCGGGCTTTGACACACCGCCGTCAC 1320
Db 1261 ATCCGGAAACAGCATGCCGGTGAATACGTTCCCGGGCTTTGACACACCGCCGTCAC 1320
Qy 1321 ACCATGGAGTGGTCTTACCCGACGAGCGNTGCCCTAACCTTCGGGGGGCAGGCCAC 1380
Db 1321 ACCATGGAGTGGTCTTACCCGACGAGCGNTGCCCTAACCTTCGGGGGGCAGGCCAC 1380
Qy 1381 GGTAGGATCAGCGACTGGGGTGAAGTCTGAACAGGTAGCGGTAGGGGAACCTGCGGTG 1440
Db 1381 GGTAGGATCAGCGACTGGGGTGAAGTCTGAACAGGTAGCGGTAGGGGAACCTGCGGTG 1440
Qy 1441 GATCACCCTCTT 1452
Db 1441 GATCACCCTCTT 1452

RESULT 2

US-10-049-228-2
; Sequence 2, Application US/10049228
; Publication No. US20030044886A1
; GENERAL INFORMATION:
; APPLICANT: TSUBOKURA, Akira
; TITLE OF INVENTION: PROCESS OF PRODUCING CAROTENOID PIGMENTS
; FILE REFERENCE: 38331-0003
; CURRENT APPLICATION NUMBER: US/10/049,228
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: PCT/JP01/04874
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: JP 2000-175124
; PRIOR FILING DATE: 2000-06-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 1426
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence corresponding to the 16S ribosomal RNA of
; OTHER INFORMATION: 81-1 strain
US-10-049-228-2

Query Match 95.0%; Score 1380; DB 14; Length 1426;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1409; Conservative 0; Mismatches 11; Indels 3; Gaps 2;
Qy 1 AGTTTGATCTCGGTCTAGAACGACGCTGGCGGAGGCTTAACACATGCAAGTCGAGCGA 60
Db 4 AGTTTGATCTCGGTCTAGAACGACGCTGGCGGAGGCTTAACACATGCAAGTCGAGCGA 63
Qy 61 GACCTTCGGTCTAGCGCGGACGCGGTAGTAACGCGTGGGAGCGTCCCTCTCTACGG 120
Db 64 GACCTTCGGTCTAGCGCGGACGCGGTAGTAACGCGTGGGAGCGTCCCTCTCTACGG 123
Qy 121 AATAGCCCGGGAACATGGGAGTAAATACCGTATACGCCCTTTGGGGGAAGATTATTCGG 180
Db 124 AATAGCCCGGGAACATGGGAGTAAATACCGTATACGCCCTTTGGGGGAAGATTATTCGG 183
Qy 181 AGAAGGATCGCCCGCGTGGATTAGGTAGTGTGGGGTAATGCCCCACCAACCGGACG 240
Db 184 AGAAGGATCGCCCGCGTGGATTAGGTAGTGTGGGGTAATGCCCCACCAACCGGACG 243
Qy 241 ATCCATAGCTGGTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGCCCCAGACTC 300
Db 244 ATCCATAGCTGGTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGCCCCAGACTC 303
Qy 301 CTACGGGAGGACGAGTGGGGAACTTTAGACAATGGGGCAACCTGATCTAGCCATGCC 360

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Db 304 CTACGGAGGACAGTGGGGAATCTTAGACAATGGGGAACCCCTGATCTAGCCATGCC 363
QY 361 GCGTGAAGTATGAAGGCTTAGGTTGTAAGCTCTTTCAGCTGGGGAAGATAATGAGCGT 420
Db 364 GCGTGAAGTATGAAGGCTTAGGTTGTAAGCTCTTTCAGCTGGGGAAGATAATGAGCGT 423
QY 421 ACCAGCAGAAGAAGCCCCGGCTAACTCCGTCCAGCAGCCGCGGTAATACGGAGGGGCT 480
Db 424 ACCAGCAGAAGAAGCCCCGGCTAACTCCGTCCAGCAGCCGCGGTAATACGGAGGGGCT 483
QY 481 AGCGTTCTCGGAATTAAGGCGGTAAGCGCAGCTAGGCGGACTGAAAGTACAGAGGTG 540
Db 484 AGCGTTCTCGGAATTAAGGCGGTAAGCGCAGCTAGGCGGACTGAAAGTACAGAGGTG 543
QY 541 AATCCAGGCTCAACCTTGGAACTGCGCTTGAACATATCAGTCTGGAGTTCGAGAGAG 600
Db 544 AATCCAGGCTCAACCTTGGAACTGCGCTTGAACATATCAGTCTGGAGTTCGAGAGAG 603
QY 601 GTGAGTGAATTCGAGGTAGAGGTGAATTCGTAGATATTCGAGAGAACACACAGTGGC 660
Db 604 GTGAGTGAATTCGAGGTAGAGGTGAATTCGTAGATATTCGAGAGAACACACAGTGGC 663
QY 661 GAAGGGGCTCACTGCTGATACGCTGAGGTGCGAAGCGTGGGAGCAACAGG 720
Db 664 GAAGGGGCTCACTGCTGATACGCTGAGGTGCGAAGCGTGGGAGCAACAGG 723
QY 721 ATTAGATACCTGGTAGTCAAGCGGTAAAGATGAATGCGAGCTGCGCAAGCATGCT 780
Db 724 ATTAGATACCTGGTAGTCAAGCGGTAAAGATGAATGCGAGCTGCGCAAGCATGCT 783
QY 781 TGTGCGGTGCACACCTTAACGATTAAGCATTCGCGTGGGAGTACGCTGCGAAGATTA 840
Db 784 TGTGCGGTGCACACCTTAACGATTAAGCATTCGCGTGGGAGTACGCTGCGAAGATTA 843
QY 841 AACTCAAGGAATTGAGGGGGCCCGCACAGCGGTGAGCATGTGTTTAATTCGAAGC 900
Db 844 AACTCAAGGAATTGAGGGGGCCCGCACAGCGGTGAGCATGTGTTTAATTCGAAGC 903
QY 901 AAGCGCAGAACCTTACCAACCTTGACATGGCAGGACCGCTGGAGAGATTCAGCTTCT 960
Db 904 AAGCGCAGAACCTTACCAACCTTGACATGGCAGGACCGCTGGAGAGATTCAGCTTCT 963
QY 961 CGTAAGAGACCTGCACACAGGTGCTGATGGCTGCTGACGCTGCTGCTGAGATGTC 1020
Db 964 CGTAAGAGACCTGCACACAGGTGCTGATGGCTGCTGACGCTGCTGCTGAGATGTC 1023
QY 1021 GGTAAAGTCCGGCAACGAGCGCAACCCACGTCCTAGTTGCCAGCAATTCAGTTGGGAAC 1080
Db 1024 GGTAAAGTCCGGCAACGAGCGCAACCCACGTCCTAGTTGCCAGC-ATTCAAGTTGGGCAC 1082
QY 1081 TCTATGAAACTCCCGATGATAGTGGGAGGAGGTGTGGATGACGTCAGTCTCTATGG 1140
Db 1083 TCTATGAAACTCCCGATGATAGTGGGAGGAGGTGTGGATGACGTCAGTCTCTATGG 1142
QY 1141 GCCTTACGGTGGGTACACAGCTGCTACATAGGTGCTGACAGTGGGTTAAATCCCAAA 1200
Db 1143 CCCTTACGGTGGGTACACAGCTGCTACATAGGTGCTGACAGTGGGTTAAATCCCAAA 1202
QY 1201 AGCCATCTCAGTTCCGATTCCTCTGCAACTCGAGGCGATGAAGTTGGAATCGCTAGTA 1260
Db 1203 AGCCATCTCAGTTCCGATTCCTCTGCAACTCGAGGCGATGAAGTTGGAATCGCTAGTA 1262
QY 1261 ATCGCGGAACAGATGCGCGGTGATACGTTCCCGGGCCCTGTACACACCGCCGCTCAC 1320
Db 1263 ATCGCGGAACAGATGCGCGGTGATACGTTCCCGGGCCCTGTACACACCGCCGCTCAC 1322
QY 1321 ACCATGGAGTGTGTTTCTACCGGACGACGNTGCGCTAAC- -TTCGGGGGCGAGGCGGCC 1378
Db 1323 ACCATGGAGTGTGTTTCTACCGGACGACGNTGCGCTAACCCCTTCGGGGGCGAGGCGGCC 1382
QY 1379 ACGGTAGGATCAGCGACTGGGGTGAAGTCTGCAACAGGTAGCC 1421
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Db 1383 ACGGTAGGATCAGCGACTGGGGTGAAGTCTGCAACAGGTAGCC 1425
RESULT 3
US-09-726-774-12
; Sequence 12, Application US/09726774
; Patent No. US20020082226A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; TITLE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09726.774
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1466
; TYPE: DNA
; ORGANISM: Bartonella henselae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1466)
; OTHER INFORMATION: n = A,T,C or G
US-09-726-774-12
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Query Match 75.3%; Score 1093.6; DB 9; Length 1466;
Best Local Similarity 87.1%; Pred. No. 1.9e-287;
Matches 1278; Conservative 0; Mismatches 161; Indels 29; Gaps 6;

QY 8 TCCTGGCTCAGAACGCTGGCGGAGGCTTAAACATGCAAGTGCAGGG-AGACCTT 66
Db 1 TCCTGGCTCAGGATGAACGCTGGCGGAGGCTTAAACATGCAAGTGCAGGGCACTCAT 60
QY 67 CGGCTCAGGCGGACGCTGAGTAACGCTGGGAAAGCTGCTCTACGGAATAGC 126
Db 61 TAGAGTACGCGGACAGCGGTGAGTAACGCTGGGAACTACCTCTTACGGAATAC 120
QY 127 CCGGGAACTGGGAGTAATACCTATACGCTTTCGGGAAAGATTTATCGGAGAGG 186
Db 121 ACAGAGAAATTTGCTTAATACCTATACCTTACTCGAGAAAGATTTATCGGAGAGG 180
QY 187 ATCGGCGCGGTGGATTAGTGTGGGTAATGGCCCAACAGCGACATCCAT 246
Db 181 ATGAGCGCGGTGGATTAGTGTGGGTAATGGCCCAACAGCGACATCCAT 240
QY 247 AGCTGTTTGGAGGATGATCAGCCACCTGGGACTGAGACACGCGCCAGACTCCTACGG 306
Db 241 AGCTGTTTGGAGGATGATCAGCCACCTGGGACTGAGACACGCGCCAGACTCCTACGG 300
QY 307 GAGCAGCATGGGGAATCTTACAAATGGGGCAACCTGATACCATGCGCGGTGA 366
Db 301 GAGCAGCATGGGGAATTTGGCAATGGGGCAACCTGATCCAGCCATGCGCGGTGA 360
QY 367 GTGATGAGCCCTAGGTTGTAAGCTCTTTCAGCTGGGAGATATGACGGTACCAGC 426
Db 361 GTGATGAGCCCTAGGTTGTAAGCTCTTTCAGCTGGGAGATATGACGGTAAACCGG 420
QY 427 AGAAGAGCCCGGCTAACTCCGTGCGCAGCAGCGCGGTAATACGGAGGGGCTAGCGTT 486
Db 421 AGAAGAGCCCGGCTAACTCCGTGCGCAGCAGCGCGGTAATACGGAGGGGCTAGCGTT 480
QY 487 GTTCGGAATTAAGCGCTAAAGCGCAGCTAGGCGGACTGAAAGTGCAGAGGTGAATCC 546
Db 481 GTTCGGAATTAAGCGCTAAAGCGCAGCTAGGCGGATTTAAAGTCAGAGGTGAATCC 540
QY 547 CAGGGCTCAACCTTGGAACTGCTTTGAAACTATCAGTCTGGAGTTCGAGAGGTGAGT 606
Db 541 CAGGGCTCAACCTTGGAACTGCTTTGAAACTATCAGTCTGGAGTTCGAGAGGTGAGT 600
QY 607 GGAATCCGAGTGTAGAGGTGAATTCGTAGATATTCGGAGGAACACCAAGTGGGAGGC 666
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Db 601 GGAATCCGAGTGTAGAGGTAATAATCGTAGATATTCGGAGGAACACCACTGGCGAGGC 660
QY 667 GGCTCACTGCTGATGACTGACCTGAGTGCAGAAAGCGTGGGAGAGCAACAGATTAGA 726
Db 661 GGCTCACTGCTGATGACTGACCTGAGTGCAGAAAGCGTGGGAGAGCAACAGATTAGA 720
QY 727 TACCTGTGTAGTCCAGCCGTAACAGATGAATCCAGACCTCGCAGCATGCTTCTCGG 786
Db 721 TACCTGTGTAGTCCAGCCGTAACAGATGAATGTAGCCGTTGGGTGGTTTACTGTCTAG 780
QY 787 TGTACACCTTAACGGATTAAAGCATTCGCGCTGGGGAGTACGGTCCGAAGATTAAACTCA 846
Db 781 TGGCGCAGCTAACGCATTAAACATTCGCGCTGGGGAGTACGGTCCGAAGATTAAACTCA 840
QY 847 AAGGAATTGACGGGGGCCCCACAAAGGGTGGAGCATGTGGTTTAAATTCGAAGCAACGGC 906
Db 841 AAGGAATTGACGGGGGCCCCACAAAGCGTGGAGCATGTGGTTTAAATTCGAAGCAACGGC 900
QY 907 CAGAACCTTACCAACCTTCACATGGCAGGACCG---CTGGAGAGATTTCAGCTTTCTCG 962
Db 901 CAGAACCTTACCAACCTTCACATGGCAGGAGTGGAGACACACCTTCCTTCAGTT 960
QY 963 TAAGAGACCTGCACACAGTGTGTCATGCTGTCAGCTCGTGTGAGATGTTTCGG 1022
Db 961 CGGCTGATCGGAGACAGTGTGTCATGCTGTCAGCTCGTGTGAGATGTTTCGG 1020
QY 1023 TTAAGTCCGCAACGAGCGCAACCCAGCTCCCTAGTTGCCAGCAATTCAGTTGGAACTC 1082
Db 1021 TTAAGTCCGCAACGAGCGCAACCCCTGCTAGTTGCCAGC-ATTTCAGTTGGCACTC 1079
QY 1083 TATGGAACCTGCGGATGATAAGTCG-GAGGAAGTGTGGATGACGTCAAGTCTCATGGG 1141
Db 1080 TAGGGGACTGCGGTTGATGAAGCGGAGAGAGAGTGGGATGACGTCAAGTCTCATGGC 1139
QY 1142 CTTACGGGTTGGGCTACACACGTGCTACAAATGGTGGTACAGTGG----- 1187
Db 1140 CTTACGGGTTGGGCTACACACGTGCTACAAATGGTGGTACAGTGGGCGAGATCGCA 1199
QY 1188 -----GTTAATCCCAAGCACTCAGTTGCGGATGCTCCTGCAACTCGAGGCA 1240
Db 1200 AGTCTGAGCTAAATCTCCAAAGCACTCAGTTGCGGATGCTCCTGCAACTCGAGTGA 1259
QY 1241 TGAAGTTGAATCGCTAGTAATCCGGAACAGCATGCGGGGTGAATACGTTCCCGGGCC 1300
Db 1260 TGAAGTTGAATCGCTAGTAATCGTGATCAGCATGCTACGGTGAATACGTTCCCGGGCC 1319
QY 1301 TTGTACACCGCCGCTACACCATGGAGTTGGTTCTACCCGACGACGNTGCGCTAACCC 1360
Db 1320 TTGTACACCGCCGCTACACCATGGAGTTGGTTCTACCCGACGACGNTGCGCTAACCC 1379
QY 1361 TTGGGGGGCAGCGCCAGGTAGATCAGCGACTGGGTGAAGTCGTAACAGGTAGC 1420
Db 1380 GCAAGGAGCGAGTACACCGGTAGGGTACGCGACITGGGTGAAGTCGTAACAGGTAGC 1439
QY 1421 CGTAGGGGAACCTCGCGCTGGATCACT 1448
Db 1440 CGTA-GGGAACCTCGCGCTGGATCACT 1466
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RESULT 4

US-09-894-467-2/c
; Sequence 2, Application US/09894467
; Patent No. US20020155519A1
; GENERAL INFORMATION:
; APPLICANT: Lindner, Luther E.
; APPLICANT: Macphree, Kathleen
; TITLE OF INVENTION: Human Blood Bacterium
; FILE REFERENCE: D6026D
; CURRENT APPLICATION NUMBER: US/09/894,467
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/187,946
; PRIOR FILING DATE: 1998-11-02

; NUMBER OF SEQ ID NOS: 20
; SEQ ID NO 2
; LENGTH: 1502
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: 58 rRNA sequence of a new human blood bacterium
US-09-894-467-2

Query Match 74.88; Score 1086.4; DB 10; Length 1502;
Best Local Similarity 86.28; Pred. No. 1.7e-285;
Matches 1245; Conservative 0; Mismatches 177; Indels 23; Gaps 3;

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QY 20 ACCAACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCGAGACCTTCGSGGTCTAGCGGC 79
Db 1502 ACCAACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCGAGACCTTCGSGGTCTAGCGGC 1443
QY 80 GGACGGGTGAGTAACCGGTGGGAACGTCGCCCTTCTACGGAATAGCCCGGGAACTGG 139
Db 1442 GGACGGGTGAGTAACCGGTGGGAACGTCGCCCTTCCGGTTCGGAATAACCTGGGAACCTAG 1383
QY 140 GAGTAATACGTAATACGCCCTTTGGGGAAAGATTATTCGGAAGAGATCGGCCCGCGTT 199
Db 1382 GGCTAATACCGGATACGCCCTTATGGGAAAGGTTTACTGCCGGAAGATCGGCCCGCGTC 1323
QY 200 GATTAGGTAGTTGGTGGGCTAATGCCACCAAGCCGACGATCCATAGCTGGTTGAGA 259
Db 1322 TGATTAGTGTGGTGGGCTAAGCGCTTACCAGGCGAGATCAGTAGCTGGTCTGAGA 1263
QY 260 GGATGATACGCCACCTGGGACTGAGACAGCGGCCAGACTCCTACGGGAGGACGACGTGG 319
Db 1262 GGATGATACGCCACCTGGGACTGAGACAGCGGCCAGACTCCTACGGGAGGACGACGTGG 1203
QY 320 GGAATCTTAGACAATGGGGCAACCTGATCTAGCCATGCGCGTGTAGTGAAGGCT 379
Db 1202 GGAATATTGGACAATGGGGCAACCTGATCCAGCCATGCGCGTGTAGTGAAGGCT 1143
QY 380 TAGGGTTGTAAGCTCTTTTCAGCTGGGAAGATATGACGTACCCAGCAGAGAGAGCCCG 439
Db 1142 TAGGGTTGTAAGCTCTTTTCAGCTGGGAAGATATGACGTACCCAGCAGAGATGAGCCCG 1083
QY 440 GCTAACTCCGTGCGCAGCAGCGCGGTAATACGGAGGGGGCTAGCGTTGTCGGAATTAAT 499
Db 1082 GCTAACTCCGTGCGCAGCAGCGCGGTAATACGAAGGGGGCTAGCGTTGTCGGAATTAAT 1023
QY 500 GGCGCTAAAGCGCAGCTAGCGGACCTGGAAGTCAGAGGTGAATCCAGGGGTCAACCT 559
Db 1022 GGCGCTAAAGCGCGCTATCGCGCTTTTAAAGTCGGGGGTGAAGCCCTGTGGCTCAACCA 963
QY 560 TGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAGAGGTGAGTGAATTCGAGTG 619
Db 962 CAGATGGCTCTCGATACCTGGGACGCTGAGTATGTTAGGTGGTGGAACTCGAGTG 903
QY 620 TAGAGTGAATTCGTAGATATTCGGAGGAACACCACTGCGGAAGGGGGCTCACTGGCTC 679
Db 902 TAGAGTGAATTCGTAGATATTCGCAAGAACACCGGTGGCGAAGGGGGCACTGGACC 843
QY 680 GATACCTGACGCTGAGGTGCGAAGCGTGGGAGCAACAGGATTAGATACCTCGTAGTC 739
Db 842 ATTACTGACGCTGAGGCGCGAAGCGTGGGAGCAACAGGATTAGATACCTCGTAGTC 783
QY 740 CAGCGCTTAACGATGAATGCCAGAGTTCGGCAAGCATGCTTGTGCTGTGCACACCTAAC 799
Db 782 CAGCGCTTAACGATGAATGCCAGAGTTCGGGCTGCTTGCACCGCAGTACGCGCAGCTAAC 723
QY 800 GATTAAAGCATTCGCGCTGGGAGTACGGTTCGCAAGATTAAACTCAAGGAATTACGG 859
Db 722 GCTTTGAGCATTCGCGCTGGGAGTACGGTTCGCAAGATTAAACTCAAGGAATTACGG 663
QY 860 GGCGCCGCAACAGCGTGGAGCATGTGTTTAAATTCGAAGCAACGCGCAGACCTTACCA 919
Db 662 GGCGCCGCAACAGCGTGGAGCATGTGTTTAAATTCGAAGCAACGCGCAGACCTTACCA 603
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Sequence 2, Application US/09902693
Patent No. US20020061561A1
GENERAL INFORMATION:
APPLICANT: MIHARA, Yasuhiro
APPLICANT: TAKEUCHI, Sonoko
APPLICANT: JOJIMA, Yasuko
APPLICANT: TONOUCHI, Naoto
APPLICANT: FUDOU, Ryosuke
APPLICANT: YOKOZEKI, Kenzo
TITLE OF INVENTION: NOVEL MICROORGANISM AND METHOD FOR PRODUCING XYLITOL OR
TITLE OF INVENTION: D-XYLULOSE
FILE REFERENCE: 0010-1015-0
CURRENT APPLICATION NUMBER: US/09/902,693
CURRENT FILING DATE: 2001-07-12
PRIORITY APPLICATION NUMBER: 09/347,001
PRIORITY FILING DATE: 1999-07-02
PRIORITY APPLICATION NUMBER: JP 10-193472
PRIORITY FILING DATE: 1998-07-08
PRIORITY APPLICATION NUMBER: JP 10-310398
PRIORITY FILING DATE: 1998-10-30
PRIORITY APPLICATION NUMBER: JP 11-12244
PRIORITY FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 1436
TYPE: DNA
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: strain S877
US-09-902-693-2

Query Match          67.1%; Score 973.6; DB 9; Length 1436;
Best Local Similarity 82.4%; Pred. No. 7.8e-255;
Matches 1186; Conservative 0; Mismatches 225; Indels 28; Gaps 5;

QY      5  TGATCTGTGCTCAGAACGCTGCGCGCAGCTTTACACATGCAAGTCGACGCGAGACC 64
Db      1  TGATCTGTGCTCAGACGCAACGCTGCGCGCATGCTTAACACATGCAAGTCGACGCAACCT 60

QY      65  TTCGGTCTTAGCGCGGCGGGTGAGTACGCGTGGGAGCGTCCCTTCTCTACGGAATA 124
Db      61  TTCGGGTTTAGTGGCGGCGGGTGAGTAAACGGGTAGGAAACCTATCCAGAGGTGGGGGATA 120

QY      125  GCCCGGGGAACTGGCGAGTAATACCGCTATACGCCCTTTGGGGGAAAG--ATTTTCGGAG 182
Db      121  ACACCGGGAACCTGGTGCTTAATACCGCATGATACCTGAGGGTTAAAGGCTTTGTGTGCT 180

QY      183  AAGGATCGCCCGCGTTGGATAGGTAGTGTGGGGTAAATGGCCCAACAGCCGACGAT 242
Db      181  TTTGAGGGGCGCTGCGTTTGATTAGCTAGTTGGTTGGTTAAAGGCTGACCAAGCGCATGAT 240

QY      243  CCATAGCTGGTTGAGAGATGATCAGCCACACTGGACTGGACTGAGACACGCCAGACTCCT 302
Db      241  CAATAGCTGGTTGAGAGATGATCAGCCACACTGGGACTGAGACACGCCAGACTCCT 300

QY      303  ACGGGAGGCAGCAGTGGGGAATCTTAGACAATGGGGGCAACCTGTATCTAGCCATGCCCG 362
Db      301  ACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGGGCAACCTGTATCCAGCAATGCCCG 360

QY      363  GTGAGTGATGAAGGCCCTTAGGGTTGTAAGCTCTTTTACGTGGGAAGATAATGACCGTAC 422
Db      361  GTGTGTGAAGAAGGCTCTTCGGATTGTAAGACACTTTTCACTAGGGAAGATGATGACGGTAC 420

QY      423  CAGCAGAAGAGCCCGGCTTAACCTCGTGCACAGCACCCGGGTAAATACGAGGGGGCTAG 482
Db      421  CTAGAGAAGAAGCCCGGGTAACTTCGTGCCAGCAGCCCGGGTAAATACGAAGGGGGCTAG 480

QY      483  CGTTGTTCCGAATTACTGGCGGTAAAGCGCACCTAGCGGACTGCGAAAGCTCGAGAGTGAA 542
Db      481  CGTTGTTCCGAATGACTGGCGGTAAAGGCGCGGTAGCGGTTTATACAGTCAGATGTGAA 540

QY      543  ATCCCAAGGGCTCAACCTTGGAACCTTGACCTTTGAAACTATCAGTCTTGAGTTCGAGAGAGT 602

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| | | | |
|------|----|--|------|
| 429 | Db | GTACCTGCAGAAAGAGCTCCGGCTAACTCCGTCGCCAGCAGCGCGGTAAATACGGAGNGG | 488 |
| 479 | QY | CTAGCGTTCTTCGGAAATTACTGGGGTAAAGCGCACGTAGGCGGACTGGAAGAGTCAGAGG | 538 |
| 489 | Db | CNAGCGTTCTTCGGAATTACTGGCGTAAAGCGCGGTAGGCGGATCGGTCAAGTTGGGG | 548 |
| 539 | QY | TGAATATCCAGGGCTCAACCTTGGAACTGCCCTTTGAAACTATCACTGCTGGAGTTCGAGAG | 598 |
| 549 | Db | TGAAGCCCGGGCTCAACCTCGGAATCGCTCCCTCAAACTACCGATCCNAGAGTTGGGAG | 608 |
| 599 | QY | AGGTGAGTGGAAATTCGAGGTAGAGGTGAAATTCGTAGATATTCGGAGGAACACCACTG | 658 |
| 609 | Db | AGGTAAACCGAATTCCTAGTGTAGAGGTGAATTCGTAGATATTCGGAGGAACACCACTG | 668 |
| 659 | QY | GGAAAGCGGCTACTGTGCTGATACTGACGTGAGGTGCGAAAGCTGGGAGGACAAACA | 718 |
| 669 | Db | GGAAAGCGGCTACTGTGACCGATACTGACGTGAGGTGCGAAAGCTGGGAGGACAAACA | 728 |
| 719 | QY | GGATTAGATACCTTGTAGTGCACCGCTAAACGATGAATCCAGACGTCGCAAGCAT - | 777 |
| 729 | Db | GGATTAGATACCTTGTAGTGCACCGCTAAACGATGAATTCGAGTGTGGGGTCTTTA | 788 |
| 778 | QY | GCTTGTCTGCTGCACACCTTAACGGATTAAGCATTCGCGCTGGGAGTACGGTCGCAAGAT | 837 |
| 789 | Db | GAGTTTCTGCTATCGCAGCTAACGCATTAAGCACCCCGCCGGGAGTACGCCGCAAGT | 848 |
| 838 | QY | TAAACTCAAGGAATGACGGGGGCCGCCACAAGGGTGGAGCATGTGTTTAATCGA | 897 |
| 849 | Db | TAAACTCAAGGAATGACGGGGGCCGCCACAAGGGTGGAGCATGTGTTTAATCGA | 908 |
| 898 | QY | AGCAAGCGCAGAACCTTACCAACCTTCACATGGCAGGACCGCTGGAGAGATT - CAGC | 955 |
| 909 | Db | ANNAACCGCAGAACCTTACAGCTCTTGACATCCCGGAGCACTTCCAGAGATGATTT | 968 |
| 956 | QY | TTTCTCGTAAGAGACCTGCACACAGTGTGCTAGTGGCTGCTCAGCTCGTCTCGTGAGA | 1015 |
| 969 | Db | TTTCACTTCGGTGACCCGGAGACAGTGTGCTAGTGGCTGCTCAGCTCGTCTCGTGAGA | 1028 |
| 1016 | QY | TGTTCCGTTAAGTCCGGCAACGAGCGCAACCCACGTCCTAGTGGCCAGCAATTCAGTTG | 1075 |
| 1029 | Db | TGTTGGGTTAAGTCCNCAACGAGCGCAACCTTCGCGCTTAGTGGCAGC - ATTTGGTTG | 1087 |
| 1076 | QY | GGAACTCTATGGAACCTGCCGATGATAAGTTCGGAGGAAGGTGTGGATGACGTCAGTCC | 1135 |
| 1088 | Db | GGGACTCTAAGGAACTGCCGATGATAAGCAGGAGGAAGGTGGGATGACGTCAGTCC | 1147 |
| 1136 | QY | CATGGCCCTTAGGGTTGGGCTACACACGCTGTACATGGTGTGAGTGGTGTGACA - | 1183 |
| 1148 | Db | CATGGCCCTTAGGGTTGGGCTACACACGCTGTACATGGTGTGAGTGGTGTGACA - | 1207 |
| 1184 | QY | -----GTGGGTTAAATCCCAAGGCATCTCAGTTGGATGTCTCTGCACTCG | 1234 |
| 1208 | Db | CCTGGAGGCTGAGCGAAATCTCTAAAGCCGTCTCAGTTGGATGTCTCTGCACTCG | 1267 |
| 1235 | QY | AGGCATGAAGTTGGAATCGCTAGTAATCGCGGAACAGCATGCCGCGGTGAATAGCTTC | 1294 |
| 1268 | Db | AGAGATGAAGTTGGAATCGCTAGTAATCGCGGAATCAGCATGCCGCGGTGAATAGCTTC | 1327 |
| 1295 | QY | CGGGCTCTTACACACCGCCCTACACCATGGAGTTGGTCTACCGACACGAGTGG | 1354 |
| 1328 | Db | CGGGNNTTATACACACCGCCCTACACCATGGAGTTGGTGTGACCCGAAGACGGTAG | 1387 |
| 1355 | QY | CTAACC - -TTCGGGGGACAGGGCCACCGTAGGATCAGCAGCTGGGGTGAAGTGTGTA | 1412 |
| 1388 | Db | CTAACCAGAAAGGGGGCAGNCGCCACGCTCAGGTCACGACTGGGGTNNNNNGTAAC | 1447 |
| 1413 | QY | AAGGTAGCGGTAGGGAACCTCGGGCTGGATCACTTCCTT | 1452 |
| 1448 | Db | ----- | 1487 |

Db 541 ATCCCCGGCTTAACCTGGGAACGTCATTTGATACGTATAGCTAGATCCGAGAGAGA 600
QY 603 GAGTGGAAATCCGAGGTAGAGTGAATTCGTAGATATTCGGAGGAACACACAGTGGCGA 662
Db 601 TTGGGAATTCCTCAGTGTAGAGGTGAATTCGTAGATATTCGGAGGAACACACAGTGGCGA 660
QY 663 AGGGGGCTCACTGCTCATACTGACGCTGAGGTGCGAAGCGTGGGAGCAACACAGAT 722
Db 661 AGGGGGCAATTCGCTCGGAACGTCGCTGAGGCGGAAGCGTGGGAGCAACACAGAT 720
QY 723 TAGATACCTGCTAGTCCACCGCTGAACGATGAATGCCAGACGCTGCGCAAGCAT-GCTT 781
Db 721 TAGATACCTGCTAGTCCACCGCTGAACGATGAATGCCAGACGCTGCGCAAGCAT-TAGTT 780
QY 782 GTCGGTGTACACCTAACCGGATTAAGCATTCGCGCTGGGGAGTACGGTGCGAAGATTA 841
Db 781 TTCAGTGTGGAAGCTAACGCTTAAGCACACCGCTGGGAGTACGACCGCAAGGTGA 840
QY 842 ACTCAAGGAATTCAGCGGGGCGCGCACAAAGCGGTGGAGCATGTGTTTAATTCGAACA 901
Db 841 ACTCAAGGAATTCAGCGGGGCGCGCACAAAGCGGTGGAGCATGTGTTTAATTCGAACA 900
QY 902 ACGGCGAGAACTTACCAACCTTGACATGCGAGGACCGCTGGAGAGATTCAGCTTCTC 961
Db 901 ACGGCGAGAACTTACCAAGCTTGTATGGGAGGACGCTGCTCAGAGATGATATTC-- 958
QY 962 GTAAGAGACCTGCACACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1021
Db 959 -TTGGACCTCCCGACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1017
QY 1022 GTTAAGTCCGGAAGGACGCAACCCAGCTCCCTAGTTGCGAGCA-ATTAGTTGGGAAC 1080
Db 1018 GTTAAGTCCGGAAGGACGCAACCCAGCTCCCTAGTTGCGAGCA-ATTAGTTGGGAAC 1077
QY 1081 TCTATGAACTGCGGATGATAAGTGCAGGAAGGTGGATGAGTCAAGTCCATCGG 1140
Db 1078 TCTAGAGAGATGCGGATGACAGCGGAGGAGTGGGATGAGTCAAGTCCATCGG 1137
QY 1141 GCCTTACGGTGGGCTACACACGCTGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1187
Db 1138 CCCTTATGACCTGGGCTACACACGCTGCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1197
QY 1188 -----GTTAATCCCAAGCAATCTCAGTTCGGATTTGCTGCTGCTGCTGCTGCTGCTGCT 1239
Db 1198 GACATGATGCGGATCTCAAAACCGCTCAGTTCGGATTCGACTCTGCACTCTGCACTCAGTGC 1257
QY 1240 ATGAAGTTGGAATGCTAGTAAATGCGGAACAGCATGCGGCTGAATACGTTCCCGGGC 1299
Db 1258 ATGAAGTTGGAATGCTAGTAAATGCGGAACAGCATGCGGCTGAATACGTTCCCGGGC 1317
QY 1300 CTTGTACACACCGGCTGCTACACCATGAGTGGTGTCTTACCGACGACGNTGCGCTAAC 1359
Db 1318 CTTGTACACACCGGCTGCTACACCATGAGTGGTGTCTTACCGACGACGNTGCGCTAAC 1377
QY 1360 CTTGGGGGGAGGGGCGGACGCTAGGATCAGCTGCTGGGTGAAGTCTGTAACAGGTA 1418
Db 1378 CGCAAGGGCGAGCGACCCAGCGTGGGCTGCGAGCTGCGGTTGAAGTCTGTAACAGGTA 1436

RESULT 7

US-09-902-693-1
; Sequence 1, Application US/09902693
; Patent No. US2002061561A1
; GENERAL INFORMATION:
; APPLICANT: MIHARA, Yasuhiro
; APPLICANT: TAKEUCHI, Sonoko
; APPLICANT: JOJIMA, Yasuko
; APPLICANT: TONOUCHI, Naoto
; APPLICANT: FUDOU, Ryosuke
; APPLICANT: YOKOZAKI, Kenzo
; TITLE OF INVENTION: NOVEL MICROORGANISM AND METHOD FOR PRODUCING XYLITOL OR
; TITLE OF INVENTION: D-XYLULOSE

FILE REFERENCE: 0010-1015-0
; CURRENT APPLICATION NUMBER: US/09/902,693
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/347,001
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: JP 10-193472
; PRIOR FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: JP 10-310398
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: JP 11-12244
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1438
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: strain P528
; OTHER INFORMATION: N at position 1365 is A, T, G, or C
US-09-902-693-1

Query Match 66.1%; Score 960.4; DB 9; Length 1438;
Best Local Similarity 82.3%; Pred. No. 3e-251;
Matches 1183; Conservative 0; Mismatches 228; Indels 27; Gaps 6;
QY 5 TGATCCTGGCTCAGAACGACGCTGGCGCAGGCTTAACACATGCAAGTCGACGCGAGACC 64
Db 1 TGATCCTGGCTCAGAGCGAACGCTGGCGCATGCTTAACACATGCAAGTCGACGCGACCT 60
QY 65 TTCGGGCTAGCGGGCGGACGGGTGAGTAACGGGTGGGAACGTCCTTCTTACGGAATA 124
Db 61 TTCGGGGTGTAGTGGCGGACGGGTGAGTAACGGGTAGGATCTATCCACGGGTGGGGATA 120
QY 125 GCCCGGGAACCTGGGAGTAATACCGTATACCCCTTTGGGGGAAAG--ATTTATCGGAG 182
Db 121 ACATGCGGAACCTGGTGTCTAATACCGCATGATACCTGAGGGTCAAAAGCGCGAGTCGCT 180
QY 183 AAGGATCGGCGCGCTTGGATAGTGTGGGGTAAATGCCCAACCAAGCCGACGAT 242
Db 181 GTGGAGGACCTGCTGCTGATAGCTGTTGTTGGGTAAAGGCTTACCAAGCGCATGAT 240
QY 243 CCATAGCTGTTGTAGAGGATGATCAGCCACACTGGGACTGAGACACGCGCCGACGCTCT 302
Db 241 CCATAGCTGTTGTAGAGGATGATCAGCCACACTGGGACTGAGACACGCGCCGACGCTCT 300
QY 303 ACGGAGGACGAGTGGGGAATCTTAGCAATGGGGGCAACCTGATCTAGCATGCGCGC 362
Db 301 ACGGAGGACGAGTGGGGAATCTTAGCAATGGGGGCAACCTGATCTAGCATGCGCGC 360
QY 363 GTGAGTGTAGAGGCTTTAGGGTTGTAAGCTCTTTTCAAGCTGGGAGGATTAATGACGGTAC 422
Db 361 GTGTGTGAAGAGGCTTTCGGATTTGAAAGCACTTTTCGACGGGAGCATGATGACGGTAC 420
QY 423 CAGCAGAGAAGACCCCGGCTAACTCCGTCGACAGACGCGCGGTAAATACGAGGGGGCTAG 482
Db 421 CCGTAGAAGAAGCCCGGCTAACTTCGTCGACAGACGCGCGGTAAATACGAGGGGGCTAG 480
QY 483 CGTTCTCGGAATTAATCTGGCGTAAAGCGACGCTAGGCGGACTGGAAAGTCAGAGGTGAA 542
Db 481 CGTTCTCGGAATTAATCTGGCGTAAAGCGGCTGTTAGGCGGTTGTTACATGCTAGATGTGAA 540
QY 543 ATCCAGGGCTCAACCTTTGGAACCTGCTTTGAACTATTCAGTCTCGAGTTCGAGAGAGT 602
Db 541 ATCCAGGGCTCAACCTTTGGAACCTGCTTTGGAACCTGCTTTGATACGTAGCTAGAGAGG 600
QY 603 GAGTGAATTCGAGTGTAGAGTGAATTCGTAGATATTCGAGGAACACACAGTGGCGA 662
Db 601 TTGTGAATTCGAGTGTAGAGTGAATTCGTAGATATTCGAGGAACACACAGTGGCGA 660
QY 663 AGGGGGCTACCTGCTCATCTACTGAGTTCGGAAGGCGTGGGAGGCAACAGGAT 722
Db 661 AGGGGGCAACCTGCTCATCTACTGAGTTCGGAAGGCGTGGGAGGCAACAGGAT 720

| | | |
|------|---|------|
| 960 | AAAGGGCGACCTGGAGCAATCCCGAAACCGTCTCAGTTCGGATTGCATCTCGAACT | 1019 |
| Db | | |
| 1233 | CGAGGGCATGAAGTTTGGAAATCGCTAGTAAATCGCGGAACAGCATGCGCGGGTGAATACGTT | 1292 |
| QY | | |
| 1020 | CGGGTGCATGAAGGCGGAATCGCTAGTAAATCGTGGATCAGCATGCCGGTGAATACGTT | 1079 |
| Db | | |
| 1293 | CCGCGGCCCTGTGTACACACCGCCGTCACACCATGGAGTTGGTCTTCCCGACGACGNTG | 1352 |
| QY | | |
| 1080 | CCCGGGCCTGTGTACACACCGCCGTCACACATGGAGTTGGTCTTCCCGACGCGCGTG | 1139 |
| Db | | |
| 1353 | CGCTAACTTCGGGGGCGACGGCGCCACGGTAGGATCAGCGACTGGGTGAAGTCGTAAAC | 1412 |
| QY | | |
| 1140 | CGCCAAACCGAAGGAGGACGGCGACCGGTAGGTTCAGCGACTGGGTGAAGTCGTAAAC | 1199 |
| Db | | |
| 1413 | AAAGGTAGCC | 1421 |
| QY | | |
| 1200 | AAAGGTAGCC | 1208 |
| Db | | |

RESULT 9

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US-09-847-513A-1
; Sequence 1, Application US/09847513A-
; Publication No. US20030104375A1
; GENERAL INFORMATION:
; APPLICANT: MBARI
; APPLICANT: DeLong, Edward
; APPLICANT: Beja, Oded
; TITLE OF INVENTION: Light-driven energy generation using proteorhodopsin
; FILE REFERENCE: MBA-101
; CURRENT APPLICATION NUMBER: US/09/847,513A
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 60/201,602
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 105184
; TYPE: DNA
; ORGANISM: Naturally occurring gamma proteobacterium
; FEATURE:
; NAME/KEY: gene
; LOCATION: (50866)..(51615)
; OTHER INFORMATION: Proteorhodopsin gene sequence.
; NAME/KEY: misc_feature
; LOCATION: (1593)..(2807)
; OTHER INFORMATION: Predicted
; PUBLICATION INFORMATION:
; AUTHORS: Beja, O., Aravind L., Koonin, E.V., Suzuki, M.T., Hadd, A., Nguyen, L.P.,
; AUTHORS: Jovanovich, S.B., Gates, C.M., Feldman, R.A., DeLong, E.F.
; TITLE: Bacterial rhodopsin: evidence for a new type of phototrophy in the sea
; JOURNAL: Science
; VOLUME: 289
; ISSUE: 5486
; PAGES: 1902-1906
; DATE: 2000-09-15
; DATABASE ACCESSION NUMBER: AF279106
; DATABASE ENTRY DATE: 2000-06-15
; RELEVANT RESIDUES: (50866)..(51615)
US-09-847-513A-1

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Query Match      60.7%; Score 881.4; DB 11; Length 105184;
Best Local Similarity 77.3%; Pred. No. 2e-229;
Matches 1179; Conservative 0; Mismatches 272; Indels 75; Gaps 6;

QY      1  AGTTTGATCCTGCTCAGAACGAGCTGGCGGAGGCTTACACATGCAAGTCGAGCGA 60
|||||
Db      97665  AGTTTGATCATGCTCAGATTGAACGCTGGCGGTAGGCTTACACATGCAAGTCGCGA 97724
|||||

QY      61  GACCTTC-----GGGTCTAGCGCGGACGGGTGAGTAAACGGTGGGAACGTGCC 109
|||||

Db      97725  GAAAGTATCTCTCGGATATCAGTATAGCGCGGACGGGTGAGTAAACGGTGTAGGAATCTACC 97784
|||||

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| | | | |
|----|-------|---|-------|
| QY | 110 | CTTCTCTACGGAATAGCCCCGGGAACATGGGGAGTAATACCGTATACGCCCTTTTGGGGAA | 169 |
| Db | 97785 | TAGTAGAAGGGATAGCCCGGGGAAACCCGGATTAATACCGTATACCTCTCTCGGGAGAA | 97844 |
| QY | 170 | AG-----ATTTATCGAGAGATCGGCCCGCTTGGATTAGTATGGTGG | 214 |
| Db | 97845 | AGAAGCGCTCTTTGAAGCTTTCCTACTAGATGAGCCTCGTAAAGATTAGCTGTGG | 97904 |
| QY | 215 | TGGGGTAAATGGCCCAACAGCGAGATCCCATAGCTGGTTTGAGAGGATGATCAGCCACA | 274 |
| Db | 97905 | TGAGTTAAAGGCTCACCAGGCGAGCATCTTTAGCTGCTGAGAGGACGATCAGCCACA | 97964 |
| QY | 275 | CTGGGACTGAGACACGGGCCAGCTCCCTACCGGAGGACAGTGGGGAACTCTTAGACAAT | 334 |
| Db | 97965 | TTGGGACTGAGACACGGGCCAGCTCCCTACCGGAGGACAGTGGGGAACTATGGACAAT | 98024 |
| QY | 335 | GGGGCAACCCCTGATCTAGCCATCGCGGTGAGTGATGAAGCCCTTAGGGTTGTAAAGCT | 394 |
| Db | 98025 | GGGCGCAGCCCTGATCTAGCCATACCGGTGTGTGAAGAAGCCCTTCGGGTGTAAAGCA | 98084 |
| QY | 395 | CTTTACAGCTGGGAAGATA-----TGACGGTACCAGACAGA | 429 |
| Db | 98085 | CTTTAGCAGGAGGAAAAAGTTAATTAATACCTTATAACCTTGATGTACCTGCAGA | 98144 |
| QY | 430 | AGAAGCCCCGGCTAACTCCGTCGCCAGCAGCCCGCTAATACGAGGGGGCTAGCGTTGTT | 489 |
| Db | 98145 | ATAAGCACCGGCTAATTCGTCGCCAGCAGCCGCTAATACGGAAGGTGCAAGCGTTAAT | 98204 |
| QY | 490 | CGGAATTACTGGGCTAAAGCCAGCTAGGCGGACTGGAAGTCTAGAGGTTGAAATCCAG | 549 |
| Db | 98205 | CGGAATTACTGGGCGCTAAAGCCGCGGTAGTGGTTGTTAAGTTTGGATTGTGAAAGCCCTG | 98264 |
| QY | 550 | GGCTCAACCTTGGAACTGCTTTGAACTATCAGTCTGGAGTTCAGAGAGGTGAGTGGA | 609 |
| Db | 98265 | GGCTCAACCTAGAACTGCTCCAAACTTAATCACTAGAGTACCTAGAGGGAGGTAGA | 98324 |
| QY | 610 | ATTCCGAGTGTAGAGTGAATTCGTAGATATTCGGAGGAAACACAGTGGGGAAGCGCGC | 669 |
| Db | 98325 | ATTCATAGTGTAGCGGTGGAATGCGTAGATATTATGAAGATACCACTGGGGAAGCGCGC | 98384 |
| QY | 670 | TCACGTGGCTGATCTAGCGCTGAGGTGCGAAGCGTGGGAGCAAAACAGANTTAGATAC | 729 |
| Db | 98385 | CTCCTGGATCTCTACTGACACTGAGGTGCGAAGCGTGGTACGCAACAGGATTAGATAC | 98444 |
| QY | 730 | CCTGTPAGTCCACGGCTAAACGATGAATCCACAGCTCGGCA-AGCATGCTTGTCGGTG | 788 |
| Db | 98445 | CTTGGTGTGTCACGCGCTAAACGATGAACACTAGCTGTGGGAGACTATGCTTTCACTG | 98504 |
| QY | 789 | TCACACCTAACGGATTAGCATTCGCGCTGGGAGTACGGTCGCAAGATTAAAACTCAAA | 848 |
| Db | 98505 | CGCAGACTAACGCTTTAAGTTTCTCGCCTGGGAGTACGCGCAAGCTAAAACTCAAA | 98564 |
| QY | 849 | GGNAITGACGGGGCCGACAAAGCGGTGGAGCATGTGTTTAATTCGAACGACGCGCA | 908 |
| Db | 98565 | TGAATTTAGCGGGACCCGACAAAGCGGTGGAGCATGTGTTTAATTCGATCGAACGCGAA | 98524 |
| QY | 909 | GAACTTACCAACCCCTTGACATGGGACGACCGCTGGAGAGATTACGCTTCTCGTAAGAG | 968 |
| Db | 98625 | AAACCTTACTACTCTTGACATCTTTGGA-GGCTCTTGAATGAGAGTGTGCCCTTTGGA | 98683 |
| QY | 969 | ACCTGCACACAGGTGCTGATGGCTGTGCTCAGCTCGTGTGAGATGTTTCGGTTAAGT | 1028 |
| Db | 98684 | ACCAAGATACAGGTGCTGATGCTGCTCAGCTCGTGTGAGATGTTTCGGTTAAGT | 98743 |
| QY | 1029 | CGGGCAACGAGGCGCAACCCACGCTCCCTAGTTGCCAGCAATTCAGTTGGGAACCTCTATGGA | 1088 |
| Db | 98744 | CGGATTAACGAGGCGCAACCCCTTACCCTTATTTGCCAGCATTCGGTTCGGGAACATAAGGG | 98803 |
| QY | 1089 | AACTGCCGATGATAGCTCGGAGGAGGCTGTGATACGCTCAGTCCATGGGCTTACG | 1148 |
| Db | 98804 | GACTGCCGCTGTAAACCCGGAGGAGGTGAGCAGCTCAAGTCAATCATGGCCCTTACG | 98863 |
| QY | 1149 | GGTTGGGCTACACACGCTGTACAATGGTGGTGACAGTGGG-----1188 | |

[illegible]

RESULT 10

```

US-10-007-725-6
; Sequence 6, Application US/10007725
; Publication No. US20020150887A1
; GENERAL INFORMATION:
; APPLICANT: Maruyama, Akihiko
; APPLICANT: Higashihara, Takanori
; APPLICANT: Kitamura, Keiko
; APPLICANT: Sunamura, Michinari
; APPLICANT: Kurane, Ryuichiro
; TITLE OF INVENTION: METHODS AND NUCLEIC ACID PROBES FOR
; TITLE OF INVENTION: MOLECULAR GENETIC ANALYSIS OF POLLUTED ENVIRONMENTS AND
; TITLE OF INVENTION: ENVIRONMENTAL SAMPLES
; FILE REFERENCE: 13558-003001
; CURRENT APPLICATION NUMBER: US/10/007,725
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: JP 341765/2000
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1532
; TYPE: DNA
; ORGANISM: Cyclocloasticus pugetii
US-10-007-725-6

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[illegible]

| | | | |
|------|----|---|------|
| 269 | QC | CACACTGGGACTGAGACACAGCCCGCAGACTCCTACGGAGGACGACGACGTGGGGAATCTT | 328 |
| 303 | DB | GCACACTGGGACTGAGACACAGCCCGCAGACTCCTACGGAGGACGACGACGTGGGGAATATTG | 362 |
| 329 | QY | GACAATGGGGCAACCCCTGATCTFAGCCATGCGCGTGAAGTGAAGGCGCTTAGGGTCTG | 388 |
| 363 | DB | CACAACTGGAGGAACCTCTGATGACGCAATGCCCGTGTGTGAAGAAGGCGCTTAGGGTCTG | 422 |
| 389 | QY | AAAGCTCTTTACGTGGGAGATAA-----TGACGGTAC | 422 |
| 423 | DB | AAAGCACTTTCACTAGGAGGAAAGTTAAAGGTAATAACCCCTTAGGCCCTGACGCTTAC | 482 |
| 423 | QY | CACGAGAAGAGCCCGGCTAACTCCGTGCCACGACGCGGCTTAATACGGAGGGGCGCTAG | 482 |
| 483 | DB | CTACAGAAGAAGCAGCGGCTAACTCCGTGCTACGACGCGGCTTAATACGGAGGGTGAAG | 542 |
| 483 | QY | CGTTGTTCGGAATTAAGTGGCGTAAAGCGCACCTFAGCGGACTGGGAAGTCAACAGTGAA | 542 |
| 543 | DB | CGTTAATCGGAATTAAGTGGCGTAAAGCGCGCAGCGGCTTAACCAAGTCAGATGTGAA | 602 |
| 543 | QY | ATCCAGGGGCTCAACCTTGAAGCTGCTTTGAAACTATCAGTCTGGAGTTCGAGAGAGGT | 602 |
| 603 | DB | AGCCCGGGCTCAACCTGGGAATGCAATTTGAACCTGGCTAGCTAGAGTGTGTAGAGGA | 662 |
| 603 | QY | GAGTGGAAATCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAACACCAAGTGGCGA | 662 |
| 663 | DB | GAGTGGAAATTCAGGTGTAGCGGTGAAATCGGTAGATATCTGAAGGAACACCAAGTGGCGA | 722 |
| 663 | QY | AGCGGCTCACTGGCTGATACCTGACGCTGAGGTGGGAAGCGTGGGAGCAACACAGGAT | 722 |
| 723 | DB | AGCGGCTCTCTGGACCAACACTGACGCTGAGGTGGGAAGCGTGGGTAGCAACCGGAT | 782 |
| 723 | QY | TAGATACCCTGGTGTACCGCGTAAACGATCAATGCCACGCTGGCAAGCATGCTTG | 782 |
| 783 | DB | TAGATACCCGGTGTACCGCGTAAACGATCAATGCCACGCTGGCAAGCATGCTTG | 842 |
| 783 | QY | TCGGTGTACACCTAACGGATTAAGCAATTCGGCTGGGAGTAGCGTTCGCAAGATTAAA | 842 |
| 843 | DB | TTAGTGGTGCA-STAGCGCAATTAAGTTGACCGCTGGGGAGTAGCGGCGCAAGGCTAAA | 901 |
| 843 | QY | CTCAAGGAATTCAGCGGGGCGGCACACAGCGGTGAGCATGTGCTTTAATTCGAAGCAA | 902 |
| 902 | DB | CTCAATATGAATTCAGCGGGGCGGCACACAGCGGTGGAGCATGTGGTTAATTCGATGCAA | 961 |
| 903 | QY | CGGCGACAACCTTACCAACCCCTTGACATGCCAGACCGCTGGAGAGATTTCAGCTTCTCG | 962 |
| 962 | DB | CGGGAAGAACCTTACCTACCCTTGACATACAGAGAACTTCTAGATAGATAGTTGGTGCT | 1021 |
| 963 | QY | TAAGAGACCTGCACACAGGTGCTGCATGGCTGCTGCAGCTCGTGTGAGATGTTCGG | 1022 |
| 1022 | DB | TCGGAACTCTGATACAGGTGCTGCATGGCTGCTGCAGCTCGTGTGAGATGTTCGG | 1081 |
| 1023 | QY | TTAAGTCCGGCAGAGCGGCAACCCAGTCCCTAGTTGCCAGCAATTCAGTTGGGAACCTC | 1082 |
| 1082 | DB | TTAAGTCCCGCTAACAGAGCGCAACCCCTTATCCTTAGTTGCTA-CCATTTAGTTGGGCACT | 1140 |
| 1083 | QY | TATGGAAATTCGCGATGATTAAGTCGGAGGAAGGTGTGGATGAGTCAAGTCCATCGGC | 1142 |
| 1141 | DB | TAGGAGACTGCCGGTGATTAACCGGAGGAAGGTGGGAGCAGCTCAAGTCATCATGGCC | 1200 |
| 1143 | QY | CTTACGGGTTGGGCTACACACGCTGCTACAATGTGTGAGCAGTGGG-----1188 | 1188 |
| 1201 | DB | CTTATGGGTAGGCTACACAGTGTCTACATATGCCCGGTACAGAGGGCGCAAACTCGCGA | 1260 |
| 1189 | QY | -----TTAATCCCAAAAGCATCTCAGTTCCGATTTGCTCTGCAACTCGAGGGCA | 1240 |
| 1261 | DB | GAGTAAGCTAATCCCTTAAAGCGGCTCTAGTCCGGATTTCAGTCTCTCAACTCGACTGCA | 1320 |
| 1241 | QY | TGAAGTTGGAATCGCTAGTAAATCCGGGAACAGATGCCGGGTGAATACGTTCCCGGCC | 1300 |
| 1321 | DB | TGAAGCTGGAATCGCTAGTAAATCCGGATCAGAAATCCCGGGTGAATTCCTCCCGGCC | 1380 |

QY 1301 TTGTACACACCGCCGTCACACCATGGAGTTGTTCTACCCGACGAGNTGCGTACCC 1360
 DB 1381 TTGTACACACCGCCGTCACACCATGGAGTTGTTCTACCCGACGAGNTGCGTACCC 1440
 QY 1361 TTCGGGGGAGCGGCGCCACGCTAGGATGAGTACGAGTGGGGTGAAGTTCGTAACAAGGTAGC 1420
 DB 1441 TTCGGGGGAGCGGCTACACCATTTGTGATTCATGACTGGGGTGAAGTTCGTAACAAGGTAGC 1500
 QY 1421 CTTAGGGGAACCTCGCGCTGGATCACCTCCTT 1452
 DB 1501 CCTAGGGGAACCTCGCGCTGGATCACCTCCTT 1532

RESULT 11

US-10-007-725-5
 ; Sequence 5, Application US/10007725
 ; Publication No. US20020150887A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Maruyama, Akibiko
 ; APPLICANT: Higashihara, Takanori
 ; APPLICANT: Kitamura, Keiko
 ; APPLICANT: Sunamura, Michinari
 ; APPLICANT: Kuran, Ryuchiro
 ; TITLE OF INVENTION: METHODS AND NUCLEIC ACID PROBES FOR
 ; TITLE OF INVENTION: MOLECULAR GENETIC ANALYSIS OF POLLUTED ENVIRONMENTS AND
 ; TITLE OF INVENTION: ENVIRONMENTAL SAMPLES
 ; FILE REFERENCE: 13558-003001
 ; CURRENT APPLICATION NUMBER: US/10/007,725
 ; CURRENT FILING DATE: 2001-11-09
 ; PRIOR APPLICATION NUMBER: JP 341765/2000
 ; PRIOR FILING DATE: 2000-11-09
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 1494
 ; TYPE: DNA
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: GR211-P1(FERM P-17394)
 US-10-007-725-5

Query Match 59.5%; Score 863.4; DB 13; Length 1494;
 Best Local Similarity 77.4%; Pred. No. 7.1e-225;
 Matches 1157; Conservative 0; Mismatches 257; Indels 80; Gaps 6;
 QY 5 TGATCTGCTCAGAACGACGCTGGCGGAGGCTTAACACATGCAAGTTCGAGCGAGACC 64
 DB 1 TTATCATGGCTCAGATTGAACGCTGGCGGAGGCTTAACACATGCAAGTTCGAGCGAAAC 60
 QY 65 TTC-----GGGTCTAGCGGCGGAGGCTGAGTAAACGCTGGGAGCGTGC 108
 DB 61 GATCCTAGCTGTAGGAGGCTGCGCGGCGGAGGCTGAGTAAACGCTGAGAGATCTGC 120
 QY 109 CCTTCTCTAGCGAATAGCCCGGAAACTGGAGTAAACGCTATACGCTATACGCTTTGGGGA 168
 DB 121 CCATTAGGGGATACCTGGGGAACCCAGGCTATACCGCATATCCCTACGCGGGA 180
 QY 169 AA-----GATTATCGGAGAGGATGCGCCCGCTGGTGGATTAGGTAGTGG 214
 DB 181 AAGCAGGGGATCTTCGGACCTTGCTGATGGATGAGTCTCGCTCGGATTAGCTTTGG 240
 QY 215 TGGGGTAATGGCCACCAAGCCGAGATCCATAGCTGGTTGAGAGATGATCAGCCACA 274
 DB 241 TGAGGTATGGCTCACCAGCGGAGCTCTCTACGGAGGAGCAGTGGGGAATCTTGACAAT 300
 QY 275 CTGGGACTGAGACAGCGCCAGACTCTACGGGAGGAGCAGTGGGGAATCTTACACAAT 334
 DB 301 CCGGGACTGAGACAGCGCCGAGCTCTCTACGGAGGAGCAGTGGGGAATCTTGACAAT 360
 QY 335 GGGGGCAACCTGTATCTAGCCATGCCGCTGAGTGAATGAAGCCCTTAGGGTTGTAAGCT 394
 DB 361 GGGGGCAACCTGTATCTAGCCATGCCGCTGAGTGAATGAAGCCCTTAGGGTTGTAAGCA 420

QY 395 CTTTCAGCTGGGAAGATAA-----TGACGGTACCAGCAGA 429
 DB 421 CTTTCAGTGGGAGGAGAGGCTTATCCTTAATACGGATGAGTACTTTGAGCTTACCTACAGA 480
 QY 430 AGAAGCCCCGGCTAACTCCGTCAGCAGCCGCGTAAATACGGAGGGGCTAGCGCTTGT 489
 DB 481 AGAAGCACCAGGCTAATTTTCGTCAGCAGCCGCGTAAATACGAAAGTTCGAGCGCTAAT 540
 QY 490 CGGAATTACTGGCGCTAAAGCGCAGCTAGCGGAGTGGAAAGTTCAGAGGTGAATTCACG 549
 DB 541 CGGAATTACTGGCGCTAAAGCGCGCTAGCGGCTTGTCTAAGTTCAGATGCTGAAAGCCCG 600
 QY 550 GGCCTAACCTTGGAACTGCTTGAAGTATACGCTGAGTTCGAGAGAGTGGAGTGA 609
 DB 601 GGCCTAACCTTGGAACTGCTTGAAGTTCGAGGCTAGATGCAAGTTCGAGAGAGTGGAG 660
 QY 610 ATTCGAGTGTAGAGGTGAATTCGTAGATATTCGAGAGGACACACCGTGGGAGAGCGCG 669
 DB 661 ATTTCCGGGTGAGCGGTGAATTCGTAGAGTTCGGAAGAACACCGTGGGAGAGCGCG 720
 QY 670 TCAGTGGCTCGATCTAGCTGAGTTCGGAAGCGTGGGAGGAGCAACAGGATTAGATAC 729
 DB 721 CTCCTGGACTGACATTCAGCTGAGTTCGGAAGCGTGGGAGGAGCAACAGGATTAGATAC 780
 QY 730 CCTGTAGTCCACCGCTAAAGCATGATGCGCAGACGTCGCGAAGC--ATGCTTCTCGT 787
 DB 781 CCTGTAGTCCACCGCTAAAGCATGCTACTAGTCTGTTGGAACTTCTAGTATCTTCTGGT 840
 QY 788 GTCACACCTAACCGATTAAAGCATTCGCGCTGGGAGTACGCTGCGAAGTAAAACTCAA 847
 DB 841 GACGAGTTAACCGGATTAAGTACCGCTGGGAGTACGCGCGCAAGTTAAACTCAA 900
 QY 848 AGGAATTGACGGGGCGCGCACAGCGTGGAGCATGTGTTTAAATTCGAGCAACAGCGC 907
 DB 901 ATGAATTGACGGGGCGCGCACAGCGTGGAGCATGTGTTTAAATTCGATGCAACGCGA 960
 QY 908 AGAACCTTACCACCTTGCATGGCAGGACCGCTGGAGAGATTCAGCTTCTCTAAGA 967
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 QY 1087 GAACTGCGGATGATTAAGTTCGAGAGGAGTGTGATGACGTCAGTCTCTATGGGCTTGA 1146
 DB 1141 GAGACTGCGGTGACAAACCGGAGGAGGAGTGGGAGCAGCTCAAGTCAATCATGCGCCCTTA 1200
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 DB 1201 CGGCTGGCTTACACACGCTGCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
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 DB 1261 AAGCAAAATCCCTTAAACTGTTCTGAGTTCGGGATGAGTTCGCAACTCTGCAACTCTGAT 1320
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22 GAACGCTGGCGGCGAGGCTTAACACATGCAAGTCGAGCGAGACCTTCGGGTCT----- 73

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| Qy | 1109 | AGAA | GGTGTGGATGAGCT | CAAGTCTCAT | TGGGCTTTAC | GGGTTGGGCT | TACACACGTGCT | 1168 | |
| Db | 1142 | AGAA | GGTGGGATGAGCT | CAAGTCA | TATCATG | GGCCCTTAC | GGCTGGGCTACACACGTGCT | 1201 | |
| Qy | 1169 | ACA | TGGTGTGACAGT | GGGTT | ----- | ----- | ATCCCAAAAGCCAT | 1206 | |
| Db | 1202 | ACA | TGTCGGTACAGAGG | GTGCC | AAAGCGGAGT | TGGAGCTAA | TCCCAAAAACCGAT | 1261 | |
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| Db | 1382 | GGAG | TGGTTC | TACCGACAGC | AGTGGCTTA | CTTCG | GGGGGAGCGGCCACAGT | 1441 | |
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| ; Sequence 5, Application US/09821016 | | | | | | | | | |
| ; Patent No. US20010046692A1 | | | | | | | | | |
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| ; APPLICANT: CANON INC. | | | | | | | | | |
| ; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same | | | | | | | | | |
| ; FILE REFERENCE: 4051021 | | | | | | | | | |
| ; CURRENT APPLICATION NUMBER: US/09/821.016 | | | | | | | | | |
| ; CURRENT FILING DATE: 2001-03-30 | | | | | | | | | |
| ; NUMBER OF SEQ ID NOS: 11 | | | | | | | | | |
| ; SOFTWARE: Microsoft Word | | | | | | | | | |
| ; SEQ ID NO 5 | | | | | | | | | |
| ; LENGTH: 1501 | | | | | | | | | |
| ; TYPE: DNA | | | | | | | | | |
| ; ORGANISM: Pseudomonas jessenii P161 ; BP-7376 | | | | | | | | | |
| ; FEATURE: | | | | | | | | | |
| US-09-821-016-5 | | | | | | | | | |
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| Qy | 74 | ---- | AGCGCGGACGGGT | GAGTAAC | CGGTGGGAACGTGCCCTTCTCT | TACGGAATAGCCCC | 129 | | |
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; Patent.No. US2002002253A1
; GENERAL INFORMATION:
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; TITLE OF INVENTION: Polyhydroxyalkanoate its manufacturing method, and micro
; TITLE OF INVENTION: these are used for the method.
; FILE REFERENCE: 4351009
; CURRENT APPLICATION NUMBER: US/09/748, 205
; CURRENT FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 1
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; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain.
US-09-748-205-1

Query Match 59.4%; Score 861.8; DB 9; Length 1501;
Best Local Similarity 77.1%; Pred. No. 1.9e-224;
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Qy 176 ATCGAGAGAGATCGGCCGCTTGGATTAGGTAGTTGGTGGGTAAATGGCCACCAAGC 235
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GenCore version 5.1.6
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24 904.8 62.3 1208 37 US-09-894-467-1
25 881.4 60.7 105184 35 US-09-847-513A-1
26 870 59.9 1532 1 PCT-US02-41014-38
27 870 59.9 1532 44 US-10-029-397A-38
28 870 59.9 1532 44 US-10-029-397B-38
29 859.8 59.9 1532 44 US-10-007-725-6
30 859.8 59.9 1532 44 US-10-049-626B-1
31 863.4 59.5 1494 44 US-10-007-725-5
32 861.8 59.4 1501 33 US-09-791-592-1
33 861.8 59.4 1501 33 US-09-791-610-1
34 861.8 59.4 1501 41 US-09-951-720-1
35 861.8 59.4 1501 46 US-10-105-305-1
36 861.8 59.4 1501 46 US-10-133-404A-1
37 861.8 59.4 1501 48 US-10-218-519-5
38 861.8 59.4 1501 48 US-10-242-696-1
39 861.8 59.4 1501 49 US-10-252-518-5
40 861.8 59.4 1501 49 US-10-266-787-5
41 861.8 59.4 1501 52 US-10-411-319-1
42 861.6 59.3 25132 62 US-60-082-302-750
43 857.6 59.1 1540 49 US-10-460-647-1
44 854.6 58.9 1535 1 PCT-US02-41014-41
45 854.6 58.9 1535 14 US-08-923-030-12

ALIGNMENTS

RESULT 1
US-09-856-640-1
; Sequence 1, Application US/09856640
; GENERAL INFORMATION:
; APPLICANT: TSUBOKURA, Akira
; APPLICANT: YONEDA, Haruyoshi
; TITLE OF INVENTION: A PIGMENT-CONTAINING SUBSTANCE FOR FEED ADDITIVES
; FILE REFERENCE: 38331-0002
; CURRENT APPLICATION NUMBER: US/09/856.640
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: PCT/JP00/06528
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 279337/1999
; PRIOR FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: DNA nucleotide sequence corresponding to 16S ribosomal RNA
; NAME/KEY: variation
; LOCATION: (1350)..(1350)
; OTHER INFORMATION: n is A or G or C or T
US-09-856-640-1

Query Match 99.9%; Score 1451; DB 35; Length 1452;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1452; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGTTTATGATCCTGGCTCAGAACGAGCTGGCGCAGGCTTAACACATGCAAGTCGACGCA 60
Db 1 AGTTTATGATCCTGGCTCAGAACGAGCTGGCGCAGGCTTAACACATGCAAGTCGACGCA 60
QY 61 GACCTTCGGGTCTAGCGGGGAGGGGTGAGTACGGTGGGAGACGTCCTTCTCTACGG 120
Db 61 GACCTTCGGGTCTAGCGGGGAGGGGTGAGTACGGTGGGAGACGTCCTTCTCTACGG 120
QY 121 ATATGCCCGGGAACCTGGAGTAATACCGCTATACGCTTTCGGGGAAGATTTATCGG 180
Db 121 ATATGCCCGGGAACCTGGAGTAATACCGCTATACGCTTTCGGGGAAGATTTATCGG 180
QY 181 AGAAGGATCGGCGCGGTTGGATTAGTGTAGTGGTGGTAAATGGCCCAACGAGCGACG 240
Db 181 AGAAGGATCGGCGCGGTTGGATTAGTGTAGTGGTGGTAAATGGCCCAACGAGCGACG 240
QY 241 ATCCATAGTGTGTTGAGAGGATGATCAGCCACCTGGGACTGAGACACGCGCCAGACTC 300
Db 241 ATCCATAGTGTGTTGAGAGGATGATCAGCCACCTGGGACTGAGACACGCGCCAGACTC 300
QY 301 CTACGGGAGCAGCAGTGGGATCTTAGACATGGGCAACCTGATCTAGCCATGCC 360
Db 301 CTACGGGAGCAGCAGTGGGATCTTAGACATGGGCAACCTGATCTAGCCATGCC 360
QY 361 GCGTGAGTGATGAAGCCCTTAGGGTTGTAAGCTCTTTCAGCTGGGGAAGATAATGACGGT 420
Db 361 GCGTGAGTGATGAAGCCCTTAGGGTTGTAAGCTCTTTCAGCTGGGGAAGATAATGACGGT 420
QY 421 ACCAGCAGAAAGAGCCCGGCTAACTCCGTCGAGCAGCCGCGGTAAATCGGAGGGGCT 480
Db 421 ACCAGCAGAAAGAGCCCGGCTAACTCCGTCGAGCAGCCGCGGTAAATCGGAGGGGCT 480
QY 481 ACGTTGTCGGAATTTACTGGGCGTAAGCGCAGCTAGGCGGACTGAAAGTCAGAGGTG 540
Db 481 ACGTTGTCGGAATTTACTGGGCGTAAGCGCAGCTAGGCGGACTGAAAGTCAGAGGTG 540
QY 541 AAATCCAGGGCTCAACCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAGAG 600
Db 541 AAATCCAGGGCTCAACCTTGGAACTGCCTTTGAAACTATCAGTCTGGAGTTCGAGAGAG 600
QY 601 GTGAGTGAATTCGAGGTGATAGGTGAATTCGTAGATATTCGGAGGAACACCGATGCC 660
Db 601 GTGAGTGAATTCGAGGTGATAGGTGAATTCGTAGATATTCGGAGGAACACCGATGCC 660
QY 661 GAAGCGGCTCACTGGCTCGATCTGAGTCACTGAGGTCCGAAAGCGTGGGAGCAAAACAGG 720
Db 661 GAAGCGGCTCACTGGCTCGATCTGAGTCACTGAGGTCCGAAAGCGTGGGAGCAAAACAGG 720
QY 721 ATTATAGTACCTCGGTAGTCCAGCGCGTAAACGATGAATGCGACAGCTCGCAAGCATGCT 780
Db 721 ATTATAGTACCTCGGTAGTCCAGCGCGTAAACGATGAATGCGACAGCTCGCAAGCATGCT 780
QY 781 TCTCGGTGTCACACCTTAACGATTAAAGCATTCGCGCTGGGAGTACGGTGCAGAGATTA 840
Db 781 TCTCGGTGTCACACCTTAACGATTAAAGCATTCGCGCTGGGAGTACGGTGCAGAGATTA 840
QY 841 AACTCAAGGAATTCGAGGGGCGCCGACAGCGGTGGAGCATGTGGTTTAAATTCGAAGC 900
Db 841 AACTCAAGGAATTCGAGGGGCGCCGACAGCGGTGGAGCATGTGGTTTAAATTCGAAGC 900
QY 901 AACGCGCAGAACCTTACCAACCTTGCATGGCAGGACCGCTGGAGAGATTCAGCTTTCT 960
Db 901 AACGCGCAGAACCTTACCAACCTTGCATGGCAGGACCGCTGGAGAGATTCAGCTTTCT 960
QY 961 CGTAAGAGACCTGCACACAGGTGCTGCATGGCTGCTGCTGAGTCTGCTGAGATGTTTC 1020
Db 961 CGTAAGAGACCTGCACACAGGTGCTGCATGGCTGCTGCTGAGTCTGCTGAGATGTTTC 1020

1201 AGCCATCTCAGTCCGATTGTCTCTGCAACTCGAGGGCATGAAGTTGGAATCGGTAGTA 1260
1261 ATCCGCGAAGACAGCATCCCGCGGTGAATACGTTCCCGGGGCTTGTACACACCCCGGTAC 1320
1261 ATCCGCGAAGACAGCATCCCGCGGTGAATACGTTCCCGGGGCTTGTACACACCCCGGTAC 1320
1321 ACCATGGAGTGGTCTTACCCGACAGCAGTGGGTAACTTCGGGGGCGACGGCGCCAC 1380
1321 ACCATGGAGTGGTCTTACCCGACAGCAGTGGGTAACTTCGGGGGCGACGGCGCCAC 1380
1381 GGTAGATCAGGACTGGGGTGAAGTCGTAACAAGTACCGGTAGGGGAACCTGCGGCTG 1440
1381 GGTAGATCAGGACTGGGGTGAAGTCGTAACAAGTACCGGTAGGGGAACCTGCGGCTG 1440
1441 GATCACTCCTT 1452
1441 GATCACTCCTT 1452

RESULT 3
US-10-049-228-2
; Sequence 2, Application US/10049228
; GENERAL INFORMATION:
; APPLICANT: TSUBOKURA, Akira
; TITLE OF INVENTION: PROCESS OF PRODUCING CAROTENOID PIGMENTS
; FILE REFERENCE: 38331-0003
; CURRENT APPLICATION NUMBER: US/10/049,228
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: PCT/JP01/04874
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: JP 2000-175124
; PRIOR FILING DATE: 2000-06-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1426
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence corresponding to the 16S ribosomal RNA of A-5
; OTHER INFORMATION: 81-1 strain
US-10-049-228-2

Query Match 95.0%; Score 1380; DB 44; Length 1426;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1409; Conservative 0; Mismatches 11; Indels 3; Gaps 2;

1 AGTTTGATCTGCTCAGAACGACGCTGGCGGCGAGCTTAACACATGCAAGTCGAGCGA 60
4 AGTTTGATCTGCTCAGAACGACGCTGGCGGCGAGCTTAACACATGCAAGTCGAGCGA 63
61 GACCTTCGGGTCTAGCGGGGACGGGTGAGTAACGCTGGGAACTGCTCTCTACGG 120
64 GACCTTCGGGTCTAGCGGGGACGGGTGAGTAACGCTGGGAACTGCTCTCTACGG 123
121 AATAGCCCGGGAACTGGGAGTAATACCGTATACGCCCTTTTGGGGGAAAGATTATCGG 180
124 AATAGCCCGGGAACTGGGAGTAATACCGTATACGCCCTTTTGGGGGAAAGATTATCGG 183
181 AGAAGATCGGCCCGGGTGGATTAGTAGTGGTGGGTGTAATGGCCGACCAAGCGGACG 240
184 AGAAGATCGGCCCGGGTGGATTAGTAGTGGTGGGTGTAATGGCCGACCAAGCGGACG 243
241 ATCCATAGCTGGTTTGGAGAGGATGATCAGCACACTGGGACTCAGACACGCGCCAGACTC 300
244 ATCCATAGCTGGTTTGGAGAGGATGATCAGCACACTGGGACTCAGACACGCGCCAGACTC 303
301 CTACGGGAGGACGAGTGGGGAATCTTAGACAATGGGGGCAACCCCTGATCTAGCCATGCC 360
304 CTACGGGAGGACGAGTGGGGAATCTTAGACAATGGGGGCAACCCCTGATCTAGCCATGCC 363

361 GGGTGAAGTATCAAGGCCCTTAGGGTTGTAAGCTCTTTTTCAGCTGGGAAAGATATGACGCT 420
364 GGGTGAAGTATCAAGGCCCTTAGGGTTGTAAGCTCTTTTTCAGCTGGGAAAGATATGACGCT 423
421 ACCAGCAGAAAGAACCCCGCTTAACCTCCGTCAGCAGCGCGGGTAAATACGAGGGGGCT 480
424 ACCAGCAGAAAGAACCCCGCTTAACCTCCGTCAGCAGCGCGGGTAAATACGAGGGGGCT 483
481 AGCGTTGTTTCGGAATTAATCTGGGGTAAAGCGCAGCTAGGCGGACTGGAAGTCAAGAGTG 540
484 AGCGTTGTTTCGGAATTAATCTGGGGTAAAGCGCAGCTAGGCGGACTGGAAGTCAAGAGTG 543
541 AATCCCGAGGCTCAACCTTGGAACTGCGCTTGAAGTATATCAGCTGCGAGTTCGAGAGAG 600
544 AATCCCGAGGCTCAACCTTGGAACTGCGCTTGAAGTATATCAGCTGCGAGTTCGAGAGAG 603
601 GTGAGTGGAAATCCCGAGTGTAGAGTGAATTCGTAGATATTCGAGGAAACACACAGTGC 660
604 GTGAGTGGAAATCCCGAGTGTAGAGTGAATTCGTAGATATTCGAGGAAACACACAGTGC 663
661 GAAGCGGCTCACTGGCTGATGACTGACGCTGAGGTGCGGAAACGCTGGGGGAGCAACAGG 720
664 GAAGCGGCTCACTGGCTGATGACTGACGCTGAGGTGCGGAAACGCTGGGGGAGCAACAGG 723
721 ATTAGATCCCTGGTGTAGTCCACCCGTAACAGTGAATCCGACGCTGCGGCAAGCATGCT 780
724 ATTAGATCCCTGGTGTAGTCCACCCGTAACAGTGAATCCGACGCTGCGGCAAGCATGCT 783
781 TGTGCTGTGTCACACCTTAACGGATTAAAGCATTCGCGCTGGGGAGTACGCTGCGCAAGTAA 840
784 TGTGCTGTGTCACACCTTAACGGATTAAAGCATTCGCGCTGGGGAGTACGCTGCGCAAGTAA 843
841 AACTCAAAGGAATTTACGGGGGCGCCACAAAGCGGTGGAGCATGTGGTTTAAATTCGAAGC 900
844 AACTCAAAGGAATTTACGGGGGCGCCACAAAGCGGTGGAGCATGTGGTTTAAATTCGAAGC 903
901 AAGCGCAGAACCTTACCAACCTTGACATGGCAGGACCGCTGAGAGATTCAGCTTCT 960
904 AAGCGCAGAACCTTACCAACCTTGACATGGCAGGACCGCTGAGAGATTCAGCTTCT 963
961 CGTAAGAGACCTGCACACAGGCTGCTGATGGCTGTGCTGAGCTGCTGCTGAGATGTTT 1020
964 CGTAAGAGACCTGCACACAGGCTGCTGATGGCTGTGCTGAGCTGCTGCTGAGATGTTT 1023
1021 GGTAAAGTCCGGCAACGAGCGCAACCCACGCTCCCTAGTTCGCCAGCAATTCAGTTGGGAC 1080
1024 GGTAAAGTCCGGCAACGAGCGCAACCCACGCTCCCTAGTTCGCCAGC-ATTTCAGTTGGGAC 1082
1081 TCTATGAACTCCCGGTGATAGCGGAGGAGGTGATGACGCTCAAGTCTCTATGG 1140
1083 TCTATGAACTCCCGGTGATAGCGGAGGAGGTGATGACGCTCAAGTCTCTATGG 1142
1141 GCCTTACGGGTTGGGTACACACGCTGCTACAATGGTGGTGACAGTGGGTTAATCCCAAA 1200
1143 CCCTTACGGGTTGGGTACACACGCTGCTACAATGGTGGTGACAGTGGGTTAATCCCAAA 1202
1201 AGCCATCTCAGTTGGGATTCCTCTGCAACTCGAGGGCATGAAGTGGATCGCTAGTA 1260
1203 AGCCATCTCAGTTGGGATTCCTCTGCAACTCGAGGGCATGAAGTGGATCGCTAGTA 1262
1261 ATCCGCGAAGCAGCATCCCGGCTGAATACGCTTCCCGGCTTGTACACACCGCCGCTAC 1320
1263 ATCCGCGAAGCAGCATCCCGGCTGAATACGCTTCCCGGCTTGTACACACCGCCGCTAC 1322
1321 ACCATGGGAGTTGGTTCTACCCGACGAGTGGGTAAACC--TTTCGGGGGGGAGCGGCGCC 1378
1323 ACCATGGGAGTTGGTTCTACCCGACGAGCTGCGCTAACCCCTTCGGGGGAGCGAGCGGCC 1382
1379 ACAGTAGGATCAGGACTGGGGTGAAGTCTGTAAACAGGTAGCC 1421
1383 ACAGTAGGATCAGGACTGGGGTGAAGTCTGTAAACAGGTAGCC 1425

RESULT 4

US-10-166-225A-12
; Sequence 12, Application US/10166225A
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/10/166,225A
; CURRENT FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Paracoccus sp. R-1512
US-10-166-225A-12

Query Match 88.5%; Score 1285.2; DB 47; Length 1404;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1343; Conservative 0; Mismatches 59; Indels 3; Gaps 2;

| QY | 30 | CGCGAGGCTTAACACATGCAAGTCGAGCGAGACCTTCGGGTCTAGCGCGGACGGGTGA | 89 |
|----|-----|--|-----|
| DB | 1 | CGCGAGGCTTAACACATGCAAGTCGAGCGAGGCTTCGGACCTAGCGCGGACGGGTGA | 60 |
| QY | 90 | GTAACGGCTGGGAAGCTGCTCTCTACGGAATAGCCCCGGGAACCTGGGAGTAATACC | 149 |
| DB | 61 | GTAACGGCTGGGAAGCTGCTCTCTACGGAATAGCCCCGGGAACCTGGGAGTAATACC | 120 |
| QY | 150 | GTAACGGCTGGGAAGCTTATCGGAGAGGATCGCGCGCTGGGATAGGTA | 209 |
| DB | 121 | GTAACGGCTGGGAAGCTTATCGGAGAGGATCGCGCGCTGGGATAGGTA | 180 |
| QY | 210 | GTTGGTGGGTAATGGCCCAAGCCAGCATCATAGCTGGTGTGAGAGGATGATCAG | 269 |
| DB | 181 | GTTGGTGGGTAATGGCCCAAGCCAGCATCATAGCTGGTGTGAGAGGATGATCAG | 240 |
| QY | 270 | CCACACTGGGACTGAGACACCGCCAGACTCCTACGGGAGGACAGTGGGGAATCTTAG | 329 |
| DB | 241 | CCACACTGGGACTGAGACACCGCCAGACTCCTACGGGAGGACAGTGGGGAATCTTAG | 300 |
| QY | 330 | ACAATGGGGCAACCTGATCTAGCCATCGCGCTGAGTGATGAAGGCTTAGGTTGTA | 389 |
| DB | 301 | ACAATGGGGCAACCTGATCTAGCCATCGCGCTGAGTGATGAAGGCTTAGGTTGTA | 360 |
| QY | 390 | AAGCTCTTACGCTGGGAAGATAATGACGGTACACGAGAGAGAGCCCGGCTAACTCCG | 449 |
| DB | 361 | AAGCTCTTACGCTGGGAAGATAATGACGGTACACGAGAGAGAGCCCGGCTAACTCCG | 420 |
| QY | 450 | TGCCAGCAGCCGCGTAAATACGAGGGGCTAGCGTTCTCGGAATTAATCGGCTAAG | 509 |
| DB | 421 | TGCCAGCAGCCGCGTAAATACGAGGGGCTAGCGTTCTCGGAATTAATCGGCTAAG | 480 |
| QY | 510 | CGCAGTAGGGGACTGAAAGTACAGAGGTGAAATCCAGGGCTCAACCTGGGAATGCC | 569 |
| DB | 481 | CGCAGTAGGGGACTGAAAGTACAGAGGTGAAATCCAGGGCTCAACCTGGGAATGCC | 540 |
| QY | 570 | TTTGAAATATCAGTCTGGAGTTCGAGAGAGTGAATTCGAGTGTAGAGGTGAA | 629 |
| DB | 541 | TCCAAAATATCAGTCTGGAGTTCGAGAGAGTGAATACCGAGTGTAGAGGTGAA | 600 |
| QY | 630 | ATTCTAGATATTCGAGAGACACACAGTGGGAGGCTCACTGGCTCGATACGTACG | 689 |
| DB | 601 | ATTCTAGATATTCGAGAGACACACAGTGGGAGGCTCACTGGCTCGATACGTACG | 660 |
| QY | 690 | CTGAGGTCGGAAGCGTGGGAGCAACAGGATAGATACCTGCTAGTCCACGCGTAA | 749 |
| DB | 661 | CTGAGGTCGGAAGCGTGGGAGCAACAGGATAGATACCTGCTAGTCCACGCGTAA | 720 |

| QY | 750 | ACGATGAATGCCAGACGTCGCGAAGCATGCTTGTGGTGTCTACACCTAACGATTAAAGCA | 809 |
|----|--|--|------|
| DB | 721 <th>ACGATGAATGCCAGTCGCGGTTCGCAATTCGGTGACACACTAACGATTAAAGCA</th> <th>780</th> | ACGATGAATGCCAGTCGCGGTTCGCAATTCGGTGACACACTAACGATTAAAGCA | 780 |
| QY | 810 <th>TTCCGCTGGGAGTACGTCGCAAGATTAAACCTCAAGGAATTCAGCGGGGCGCGCAC</th> <th>869</th> | TTCCGCTGGGAGTACGTCGCAAGATTAAACCTCAAGGAATTCAGCGGGGCGCGCAC | 869 |
| DB | 781 <th>TTCCGCTGGGAGTACGTCGCAAGATTAAACCTCAAGGAATTCAGCGGGGCGCGCAC</th> <th>840</th> | TTCCGCTGGGAGTACGTCGCAAGATTAAACCTCAAGGAATTCAGCGGGGCGCGCAC | 840 |
| QY | 870 <th>AAGCGGTGAGCATGTGGTTTAAATTCGAAGCAACCGCAGAACCTTACCAACCTTGACA</th> <th>929</th> | AAGCGGTGAGCATGTGGTTTAAATTCGAAGCAACCGCAGAACCTTACCAACCTTGACA | 929 |
| DB | 841 <th>AAGCGGTGAGCATGTGGTTTAAATTCGAAGCAACCGCAGAACCTTACCAACCTTGACA</th> <th>900</th> | AAGCGGTGAGCATGTGGTTTAAATTCGAAGCAACCGCAGAACCTTACCAACCTTGACA | 900 |
| QY | 930 <th>TGGCAGGACCGCTGGAGAGATTCAGCTTCTCGTAAGAGACCTGCACAGTGTGCTAT</th> <th>989</th> | TGGCAGGACCGCTGGAGAGATTCAGCTTCTCGTAAGAGACCTGCACAGTGTGCTAT | 989 |
| DB | 901 <th>TCCCTGGACATCCCGAGAGATCGGCTTTTAACTTCGGTGACGAGAGAGTGTGCTAT</th> <th>960</th> | TCCCTGGACATCCCGAGAGATCGGCTTTTAACTTCGGTGACGAGAGAGTGTGCTAT | 960 |
| QY | 990 <th>GGCTGTCTGAGCTGCTGTCGAGATGTCGGTTAAAGTCGCGCAACGAGCGCAACCCAC</th> <th>1049</th> | GGCTGTCTGAGCTGCTGTCGAGATGTCGGTTAAAGTCGCGCAACGAGCGCAACCCAC | 1049 |
| DB | 961 <th>GGCTGTCTGAGCTGCTGTCGAGATGTCGGTTAAAGTCGCGCAACGAGCGCAACCCAC</th> <th>1020</th> | GGCTGTCTGAGCTGCTGTCGAGATGTCGGTTAAAGTCGCGCAACGAGCGCAACCCAC | 1020 |
| QY | 1050 <th>GTCCCTAGTGGCAGCAATTCAGTTGGGAACCTCTATGGAACCTGCCGATGATAGTCGA</th> <th>1109</th> | GTCCCTAGTGGCAGCAATTCAGTTGGGAACCTCTATGGAACCTGCCGATGATAGTCGA | 1109 |
| DB | 1021 <th>GTCCCTAGTGGCAGC-ATTCAAGTTGGGCACTCTATGGAACCTGCCGATGATAGTCGA</th> <th>1079</th> | GTCCCTAGTGGCAGC-ATTCAAGTTGGGCACTCTATGGAACCTGCCGATGATAGTCGA | 1079 |
| QY | 1110 <th>GGAAGGTGGATGACGTCAGTCTCTATGGGCTTACCGGTTGGGCTACACAGTGTGTA</th> <th>1169</th> | GGAAGGTGGATGACGTCAGTCTCTATGGGCTTACCGGTTGGGCTACACAGTGTGTA | 1169 |
| DB | 1080 <th>GGAAGGTGGATGACGTCAGTCTCTATGGGCTTACCGGTTGGGCTACACAGTGTGTA</th> <th>1139</th> | GGAAGGTGGATGACGTCAGTCTCTATGGGCTTACCGGTTGGGCTACACAGTGTGTA | 1139 |
| QY | 1170 <th>CAATGGTGGTACAGTGGGTTAATCCCAAAAGCCATCTCAGTTCGGATTGCTCTGCA</th> <th>1229</th> | CAATGGTGGTACAGTGGGTTAATCCCAAAAGCCATCTCAGTTCGGATTGCTCTGCA | 1229 |
| DB | 1140 <th>CAATGGTGGTACAGTGGGTTAATCCCAAAAGCCATCTCAGTTCGGATTGCTCTGCA</th> <th>1199</th> | CAATGGTGGTACAGTGGGTTAATCCCAAAAGCCATCTCAGTTCGGATTGCTCTGCA | 1199 |
| QY | 1230 <th>ACTCAGGCGCATGAAAGTTGGAATCGCTAGTAATCGCGAAGCATGCCGCGTGAATAC</th> <th>1289</th> | ACTCAGGCGCATGAAAGTTGGAATCGCTAGTAATCGCGAAGCATGCCGCGTGAATAC | 1289 |
| DB | 1200 <th>ACTCAGGCGCATGAAAGTTGGAATCGCTAGTAATCGCGAAGCATGCCGCGTGAATAC</th> <th>1259</th> | ACTCAGGCGCATGAAAGTTGGAATCGCTAGTAATCGCGAAGCATGCCGCGTGAATAC | 1259 |
| QY | 1290 <th>GTTCGCGGCGCTTGTACACACCGCGCTCACACCATGGAGTGGTTCCTACCGGAGCG</th> <th>1349</th> | GTTCGCGGCGCTTGTACACACCGCGCTCACACCATGGAGTGGTTCCTACCGGAGCG | 1349 |
| DB | 1260 <th>GTTCGCGGCGCTTGTACACACCGCGCTCACACCATGGAGTGGTTCCTACCGGAGCG</th> <th>1319</th> | GTTCGCGGCGCTTGTACACACCGCGCTCACACCATGGAGTGGTTCCTACCGGAGCG | 1319 |
| QY | 1350 <th>NTGCGCTAAC-TCGCGGGGCGAGCGCGGCTGAGTATCAGGATCGGCTGGAAGTC</th> <th>1407</th> | NTGCGCTAAC-TCGCGGGGCGAGCGCGGCTGAGTATCAGGATCGGCTGGAAGTC | 1407 |
| DB | 1320 <th>CTGCGCTAACCTTCGGGAGCGAGCGGCTGAGTATCAGGATCGGCTGGAAGTC</th> <th>1379</th> | CTGCGCTAACCTTCGGGAGCGAGCGGCTGAGTATCAGGATCGGCTGGAAGTC | 1379 |
| QY | 1408 <th>GTAACAAGGTAGCGGTAGGGGAACC</th> <th>1432</th> | GTAACAAGGTAGCGGTAGGGGAACC | 1432 |
| DB | 1380 <th>GTAACAAGGTAGCGGTAGGGGAACC</th> <th>1404</th> | GTAACAAGGTAGCGGTAGGGGAACC | 1404 |

RESULT 5

US-60-296-299-12
; Sequence 12, Application US/60296299
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne
; APPLICANT: YELISEEV, Alexei
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/60/296,299
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Paracoccus sp. R-1512
US-60-296-299-12

Query Match

88.5%; Score 1285.2; DB 84; Length 1404;

| | Best Local Similarity | 95.6% | Pred. No. 0; | Mismatches | 59; | Indels | 3; | Gaps | 2; |
|----|-----------------------|--------------|--------------|--|------|--------|----|------|----|
| | Matches 1343; | Conservative | 0; | | | | | | |
| QY | 30 | GC | GC | AGGCTTACACATGCAAGTCCAGCGAGACCTTCGGGTCTAGCGCGGACGGGTGA | 89 | | | | |
| Db | 1 | GC | GC | AGGCTTACACATGCAAGTCCAGCGAGGCTCTTCGACCTAGCGCGGACGGGTGA | 60 | | | | |
| QY | 90 | GT | AA | CGGTGGGAACGTGCCCTTCTCTACGGAAATACCCCGGAAACTGGGAGTAATACC | 149 | | | | |
| Db | 61 | GT | AA | CGGTGGGAACGTGCCCTTTCGTACGGAATAGTCCCGGAAACTGGGTTTAATACC | 120 | | | | |
| QY | 150 | GT | AT | AGCCCTTTGGGGGAAAGATTATCGGAGAAAGATCGGCCCGCTTGGATTAGGTA | 209 | | | | |
| Db | 121 | GT | AT | GTGCCCTACGGGGGAAAGATTATCGGAAAGATCGGCCCGCTTGGATTAGGTA | 180 | | | | |
| QY | 210 | GT | TG | TGGGTAAATGCCACCAAGCGAGATCCATAGCTGTTTGAGAGGATGATCAG | 269 | | | | |
| Db | 181 | GT | TG | TGGGTAAATGGCCTACCAAGCGGAGATCCATAGCTGTTTGAGAGGATGATCAG | 240 | | | | |
| QY | 270 | CC | AC | TGGGACTGAGACACGGCCACAGACTCTACGGGAGGACAGTGGGGAACTTAG | 329 | | | | |
| Db | 241 | CC | AC | TGGGACTGAGACACGGCCACAGACTCTACGGGAGGACAGTGGGAACTTAG | 300 | | | | |
| QY | 330 | ACA | AT | GGGGCAACCTTGATCTAGCCATGCCGCTGAGTGATGAAGCCCTTAGGGTTGA | 389 | | | | |
| Db | 301 | ACA | AT | GGGGCAACCTTGATCTAGCCATGCCGCTGAGTGATGAAGCCCTTAGGGTTGA | 360 | | | | |
| QY | 390 | AA | GC | CTTTTCAGCTGGGAAGATAATGACGTACACGAGAAAGCCCGCTAACTCCG | 449 | | | | |
| Db | 361 | AA | GC | CTTTTCAGCTGGGAAGATAATGACGTACACGAGAAAGCCCGCTAACTCCG | 420 | | | | |
| QY | 450 | TG | CC | ACGACGCGCGGTAAATACGGAGGGGCTAGCGTTTTCGGAATTACTGGGCGTAAAG | 509 | | | | |
| Db | 421 | TG | CC | ACGACGCGCGGTAAATACGGAGGGGCTAGCGTTTTCGGAATTACTGGGCGTAAAG | 480 | | | | |
| QY | 510 | CG | AC | GTTAGCGGACTGGAAGTTCAGAGGTAAATCCAGGGCTCAACCTTGAACCTGCC | 569 | | | | |
| Db | 481 | CG | AC | GTTAGCGGACTGGAAGTTCAGAGGTAAATCCCGGGGCTCAACCTTGAACCTGCC | 540 | | | | |
| QY | 570 | TT | TG | AACTATACGTCTGGAGTTCGAGAGAGTGTAGTGAATCCGAGTGTAGAGGTGA | 629 | | | | |
| Db | 541 | TC | CA | AAACTATACGTCTGGAGTTCGAGAGAGTGTAGTGAATCCGAGTGTAGAGGTGA | 600 | | | | |
| QY | 630 | AT | TC | GATAGATTTCGGAGAACACCACTGCGAGGCGGCTCACTGCTCGATACTGACG | 689 | | | | |
| Db | 601 | AT | TC | GATAGATTTCGGTGGAAACACCACTGCGAGGCGGCTCACTGCTCGATACTGACG | 660 | | | | |
| QY | 690 | CT | GA | GTGCGAAAGCTGGGGAGCAACACGATTAGATACCTGGTGTAGTCCACGCCGTAA | 749 | | | | |
| Db | 661 | CT | GA | GTGCGAAAGCTGGGGAGCAACACGATTAGATACCTGGTGTAGTCCACGCCGTAA | 720 | | | | |
| QY | 750 | AC | GA | TGAATCCACAGACTCGGCAAGCATGTTGCGGTGTACACCTTAACGGATTAAACA | 809 | | | | |
| Db | 721 | AC | GA | TGAATCCACAGACTCGGCGGTTGATGCAATTCGTTGACACACCTTAACGGATTAAACA | 780 | | | | |
| QY | 810 | TT | CC | CGCTGGGAGTACGGTCGCAAGATTAAACTCAAAGGAATGACGGGGCCCGCAC | 869 | | | | |
| Db | 781 | TT | CC | CGCTGGGAGTACGGTCGCAAGATTAAACTCAAAGGAATGACGGGGCCCGCAC | 840 | | | | |
| QY | 870 | AA | GG | GTTGAGCATGTGGTTTAATTCGAAGCAACGCGCAGAACCTTACCAACCTTGACA | 929 | | | | |
| Db | 841 | AA | GG | GTTGAGCATGTGGTTTAATTCGAAGCAACGCGCAGAACCTTACCAACCTTGACA | 900 | | | | |
| QY | 930 | TG | GC | CAGCCGCTGGAGAGATTACGCTTTCTCGTAAGAGACCTGCACACAGGTCTGCAT | 989 | | | | |
| Db | 901 | TC | CT | TGGACATCCGAGAGATCGGGCTTTTCACTTCGGTGCACGAGACAGGTCTGCAT | 960 | | | | |
| QY | 990 | GG | GT | GTGCTCAGCTCGGTGCTGAGATGTTCCGTTAAGTCGGGCAACAGAGCGCAACCCAC | 1049 | | | | |
| Db | 961 | GG | GT | GTGCTCAGCTCGGTGCTGAGATGTTCCGTTAAGTCGGGCAACAGAGCGCAACCCAC | 1020 | | | | |
| QY | 1050 | GT | CC | CTAGTTGCCAGCAATTACGTTGGGAACCTTATCGAAACTCCCGATGATAAGTCGGA | 1109 | | | | |

RESULT 6

```

US-09-735-567-1/C
; Sequence 1, Application US/09735567
; GENERAL INFORMATION:
; APPLICANT: Bramucci, Michael
; TITLE OF INVENTION: Nucleic Acid Fragments for the Identification of Bacteria in
; TITLE OF INVENTION: Industrial Wastewater Bioreactors
; FILE REFERENCE: BC1033 US NA
; CURRENT APPLICATION NUMBER: US/09/735,567
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/171,140
; PRIOR FILING DATE: 16 DECEMBER 1999
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1385
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Paracoccus sp
; OTHER INFORMATION: Nucleotide sequence of 16S rDNA corresponding to strain EMB 1
US-09-735-567-1

```

| | Query Match | 83.5%; | Score 1212.6; | DB 32; | Length 1385; |
|----|----------------------------|---|---------------|------------|--------------|
| | Best Local Similarity | 93.6%; | Pred. No. 0; | | |
| | Matches 1297; Conservative | 0; | Mismatches | 85; Indels | 4; Gaps |
| Qy | 18 | GAAGCACGCTGGCGCAGCCTTAACACATGCAGTTCGAGCGAGACCTTCGGGTCTAGCG | 77 | | |
| Dd | 1385 | GAACGAACGCTGGCGCAGGCCCTAACACATGCAAGTCGAGCGAGGACTTCGGTGCTTAGCG | 1326 | | |
| Qy | 78 | GCGACCGGGTGAGTAACCGCTGGGAACGTCGCCCTTCTACGGAATAAGCCCCGGGAAACT | 137 | | |
| Dd | 1325 | GCGACCGGGTGAGTAACCGCTGGGAACGTCGCCCTTCTTCGGNATAGCCCTGGGAAACT | 1266 | | |
| Qy | 138 | GGGAGTAATAACCGTATACGC-CCTTTGGGGGAAGAATTATTCGGAGAAGATCGGCCCGC | 196 | | |
| Dd | 1265 | GGGNGTAATACCGATACGCTCTTTTGGAGAAGATTATTCGGCGAAGATCGGCCCGC | 1206 | | |
| Qy | 197 | GTTCGGATTAGTGTGGTGGGTAATGGCCCCACCAGCGCAGATCCATAGCTGTGTTTG | 256 | | |
| Dd | 1205 | GTTCGGATTAGTGTGGTGGGTAATGGCTCTACCAAGCGCAGATCCATAGCTGTGTTTG | 1146 | | |
| Qy | 257 | AGAGGATGATCGCCACACTGGGNACTGAGACGCGCCCACNACTCCTACGGGAGGCACGAG | 316 | | |
| Dd | 1145 | AGAGGATGATCGCCACACTGGGNACTGAGACGCGCCCACNACTCCTACGGGAGGCACGAG | 1086 | | |

QY 317 TGGGAATCTTAGCAATGGGGCAACCCCTGATAGCCATGCCGCTGAGTGATGAAGG 376
DB |||||||
QY 1085 TGGGAATCTTAGCAATGGGGCAACCCCTGATAGCCATGCCGCTGAGTGATGAAGG 1026
DB |||||||
QY 377 CCTTAGGGTTCTAAAGCTCTTTACGCTGGGAGATAATGACGGTACCAAGAGAACCC 436
DB |||||||
QY 1025 CCTTAGGGTTCTAAAGCTCTTTACGCTGGGAGATAATGACGGTACCAAGAGAACCC 966
DB |||||||
QY 437 CCGCTAACTCCGTCGACGACCGCGCTAATACGGAGGGGCTAGCCTGTTCCGAATTT 496
DB |||||||
QY 965 CCGCTAACTCCGTCGACGACCGCGCTAATACGGAGGGGCTAGCCTGTTCCGAATTT 906
DB |||||||
QY 497 ACTGGCGCTAAAGCGCAGTGGGCGACTGGAAGTCAAGAGTGAAGTAAATCCAGAGGCTCAA 556
DB |||||||
QY 905 ACTGGCGCTAAAGCGCAGTGGGCGACTGGAAGTGAAGTGGGGTGAATCCCGGGCTCAA 846
DB |||||||
QY 557 CCTTGGAACTCCCTTTGAAACTATCAGTCTGGAGTTCGAGAGAGTGAAGTGAATTCGGA 616
DB |||||||
QY 845 CCGCGAACTCCCTTCAAACCTGTCAGTCTGGAGTTCGAGAGAGTGAAGTGAATTCGGA 786
DB |||||||
QY 617 GTGTAGAGTGAATTCGATATATTCGAGAGACACCAAGTGGCGAAGCGGCTCACTGG 676
DB |||||||
QY 785 GTGTAGAGTGAATTCGATATATTCGAGAGACACCAAGTGGCGAAGCGGCTCACTGG 726
DB |||||||
QY 677 CTCGATCTGACGCTGAGGTGCGAAAGCGTGGGAGCAACAGAGATTAGATACCTGCTGA 736
DB |||||||
QY 725 CTCGATCTGACGCTGAGGTGCGAAAGCGTGGGAGCAACAGAGATTAGATACCTGCTGA 666
DB |||||||
QY 737 GTCCACGCGCTAAACGATGAATGCCAGACGCTCGGCAAGCATGCTTGTGCGTGTACACCT 796
DB |||||||
QY 665 GTCCACGCGCTAAACGATGAATGCCAGTCTCGGCGACGATGCTGCTCGGTGACACCT 606
DB |||||||
QY 797 AACGGATTAAGCATTCGCCCTTGGGGAGTACGGTGCAGAGATTAAGTGAAGGAAATGA 856
DB |||||||
QY 605 AACGGATTAAGCATTCGCCCTTGGGGAGTACGGTGCAGAGATTAAGTGAAGGAAATGA 546
DB |||||||
QY 857 CGGGGCGCCGACAGCGGTGGAGCATGCTGTTAATTCGAAGCAACCGCAGACCTTA 916
DB |||||||
QY 545 CGGGGCGCCGACAGCGGTGGAGCATGCTGTTAATTCGAAGCAACCGCAGACCTTA 486
DB |||||||
QY 917 CCAACCTCTGACATCGGAGGACCGCTGGAGAGATTCAGCTTCTCGTGAAGACGCTGAC 976
DB |||||||
QY 485 CCAACCTCTGACATCGGAGGACCGCACCAGAGATGGTGTTCCTCTTCGGGCGGGAG 426
DB |||||||
QY 977 ACAGTGTGTCATGCTGCTCAGCTGCTGCTGAGATGTTGCGTTAAGTTCGCGCAAC 1036
DB |||||||
QY 425 ACAGTGTGTCATGCTGCTCAGCTGCTGCTGAGATGTTGCGTTAAGTTCGCGCAAC 366
DB |||||||
QY 1037 GAGCGCAACCCACGTCCTTAGTTCGACCAATTCAGTTGGGAATCTATGGAACCTGCGG 1096
DB |||||||
QY 365 GAGCGCAACCCACACTTCCAGTTGCCATPC - ATTCCGTTGGGCATCTCTGGAAGAACCTGCGG 307
DB |||||||
QY 1097 ATGATAAGTCGGAGGAGGTGATGACGTCAGTCTCATGGGCTTACGGGTTGGGC 1156
DB |||||||
QY 306 ATGATAAGTCGGAGGAGGTGATGACGTCAGTCTCATGGGCTTACGGGTTGGGC 247
DB |||||||
QY 1157 TACACAGTGTCTCAATGGTGGTGACAGTGGGTTAATCCCAAGGCAATCTCATGTTGGG 1216
DB |||||||
QY 246 TACACAGTGTCTCAATGGGCGGTGACAATGGGTTAATCCCAAGGCAATCTCATGTTGGG 187
DB |||||||
QY 1217 ATTCTCTCTCAACTCGAGGGCATGAATGGATGGAATCGCTAGTATTCGCGGAACAGCATG 1276
DB |||||||
QY 186 ATTGGGTTCTCAACTCGACCCCATGAATGGATGGATCGCTAGTATTCGCGGAACAGCATG 127
DB |||||||
QY 1277 CCGGGTGAATACACTTCCGGGCTTGTACACACCGCCGTCACACCATGGAGTTGGTT 1336
DB |||||||
QY 126 CCGGGTGAATACACTTCCGGGCTTGTACACACCGCCGTCACACCATGGAGTTGGTT 67
DB |||||||
QY 1337 CTACCCGACGACGNTGCGCTAACCC - TTTCGGGGGCGAGCGGCCGACCGGTAGGATCAGCGA 1394
DB |||||||
QY 66 CTACCCGACGCGCTGCGCTAACCCCTTACGGGAGGACGCGGACCGGTAGGCTCAGCGA 7

QY 1395 CTGGGG 1400
DB |||||||
DB 6 CTGGGG 1
RESULT 7
US-60-171-140-1/c
; Sequence 1, Application US/60171140
; GENERAL INFORMATION:
; APPLICANT: Bramucci, Michael
; TITLE OF INVENTION: Nucleic Acid Fragments for the Identification of Bacteria in
; TITLE OF INVENTION: Industrial Wastewater Bio-reactors
; FILE REFERENCE: BC1033 US PV
; CURRENT APPLICATION NUMBER: US/60/171,140
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1385
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Paracoccus sp
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence of 16S rDNA corresponding to strain EMBE
US-60-171-140-1
Query Match 83.5%; Score 1212.6; DB 71; Length 1385;
Best Local Similarity 93.6%; Pred. No. 0;
Matches 1297; Conservative 0; Mismatches 85; Indels 4; Gaps 3;
QY 18 GAACGAACGCTGGCGGAGGCTTAACACATGCAAGTCGAGCGAGACCTTCGGGTCTAGCG 77
DB 1385 GAACGAACGCTGGCGGAGGCTTAACACATGCAAGTCGAGCGAGACCTTCGGGTCTAGCG 1326
QY 78 GCGGACGCGGTGAGTAACGCTGGGAACTGCTCTCTACGAAATAGCCCCGGGAAACT 137
DB 1325 GCGGACGCGGTGAGTAACGCTGGGAACTGCTCTCTCTCGAATAGCCCCGGGAAACT 1266
QY 138 GGGAGTAATACCGTATACGC - CCTTTGGGGGAAAGATTATTCGGAGAGAGATTCGCCCGC 196
DB 1265 GGGAGTAATACCGTATACGCCTTTTGGAGAAAGATTATTCGGGGAAGGATTCGCCCGC 1206
QY 197 GTTGATTAGTAGTGTGGGTAAATGGCCACCAAGCCGACGATCCATAGCTGGTTG 256
DB 1205 GTTGATTAGTAGTGTGGGTAAATGGCCACCAAGCCGACGATCCATAGCTGGTTG 1146
QY 257 AGAGGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTCTACGGAGGCGAGCAG 316
DB 1145 AGAGGATGATCAGCCACACTGGGACTGAGACACGCGCCAGACTCTACGGAGGCGAGCAG 1086
QY 317 TGGGAATCTTAGCAATGGGGCAACCCCTGATAGCCATGCCGCTGAGTGATGAAGG 376
DB 1085 TGGGAATCTTAGCAATGGGGCAACCCCTGATAGCCATGCCGCTGAGTGATGAAGG 1026
QY 377 CCTTAGGGTTCTAAAGCTCTTTACGCTGGGAGATAATGACGGTACCAAGAGAACCC 436
DB 1025 CCTTAGGGTTCTAAAGCTCTTTACGCTGGGAGATAATGACGGTACCAAGAGAACCC 966
QY 437 CCGCTAACTCCGTCGACGACCGCGCTAATACGGAGGGGCTAGCCTGTTCCGAATTT 496
DB 965 CCGCTAACTCCGTCGACGACCGCGCTAATACGGAGGGGCTAGCCTGTTCCGAATTT 906
QY 497 ACTGGCGCTAAAGCGCAGTGGGCGACTGGAAGTGAAGTGAAGTAAATCCAGAGGCTCAA 556
DB 905 ACTGGCGCTAAAGCGCAGTGGGCGACTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 846
QY 557 CCTTGGAACTCCCTTTGAAACTATCAGTCTGGAGTTCGAGAGAGTGAAGTGAATTCGGA 616
DB 845 CCGCGAACTCCCTTCAAACCTGTCAGTCTGGAGTTCGAGAGAGTGAAGTGAATTCGGA 786
QY 617 GTGTAGAGTGAATTCGATATATTCGAGAGACACCAAGTGGCGAAGCGGCTCACTGG 676
DB |||||||

| | | | |
|----|-------|---|-------|
| Db | 17698 | GGATGATGAGCCCGGTTGGGATTAGCTAGTTGGTGGGTAAGGCCCTACCAAGCGAGC | 17757 |
| Qy | 241 | ATCCATAGCTGTTTCAGAGGATGATCAGCCACATCGGACATGAGACACAGGCCCGCAGATC | 300 |
| Db | 17758 | ATCCATAGCTGGTCTGAGAGGATGATCAGCCACATGGGACATGAGACACAGGCCCGCAATC | 17817 |
| Qy | 301 | CTACGGGAGCAGCAGTGGGGAATCTTAGACAATGGGGCAACCCCTGATCTAGCCATGCC | 360 |
| Db | 17818 | CTACGGGAGCAGCAGTGGGGAATATTGGACAATGGCGCAAGCCTGATCCAGCCATGCC | 17877 |
| Qy | 361 | GCGTGAGTGTGAAGCCCTTAGGTTGTAAGCTCTTCAGCTGGGGAAGATAATCAGGT | 420 |
| Db | 17878 | GCGTGAGTGTGAAGCCCTTAGGTTGTAAGCTCTTCACCGATGAAGATAATCAGGT | 17937 |
| Qy | 421 | ACCAGCAGAAGAGCCCGCTTAACCTCGCTGCCAGCAGCCGGGTAAATACGAGGGGGCT | 480 |
| Db | 17938 | AGTCGGAGAAGAAGCCCGCTTAACCTCGCTGCCAGCAGCCGGGTAAATACGAAGGGGT | 17997 |
| Qy | 481 | AGCGTTGTCGGAATTACTTGGGGGTAAAGCGGCACGTAGCGGACATGGAAGTCAGAGTG | 540 |
| Db | 17998 | AGCGTTGTCGGAATTACTTGGCGTAAAGCGCACGTAGCGGATATTAAAGTCAGGGGTG | 18057 |
| Qy | 541 | AAATCCCGAGGCTCAACCTTGAACCTCTTGAACCTATCAGTCTGGAGTTCGAGAGAG | 600 |
| Db | 18058 | AAATCCCGCAGCTCAACTCGGGAAGCTCTTTGATACTGGGTATCTTGAGTATGAAGAG | 18117 |
| Qy | 601 | GTGAGTGGAAATTCGAGTGTAGAGTGAATTCGTGTAGATATTTCGGAGCAACACCGATGC | 660 |
| Db | 18118 | GTAAAGTGGAAATTCGAGTGTAGAGTGAATTCGTGTAGATATTTCGGAGCAACACCGATGC | 18177 |

| | | | |
|-------|--|---|-------|
| 18178 | GAAGGCGGCTTACGTCGGTCCATATACGACGCTGAGGTGCGGAAAGCTGTGGGAGCAACACAGG | 18223 | |
| QY | 721 | ATTAGATACCCCTGGTAGTCCACGCGCTAAACGATGAATGCCAGACGTGGCGCAAGCATGCT | 780 |
| Db | 18238 | ATTAGATACCCCTGGTAGTCCACGCGCTAAACGATGAATGTTAGCCGTGGCGCAGTATACT | 18297 |
| QY | 781 | TGTCGGTGTACACACCTAACGGATTAAAGCATTCGCGCTGGGAGTACGGTGCAGAAATTA | 840 |
| Db | 18298 | GTTCGGTGGCGCAGCTAACGCATTAACCATTCGCGCTGGGAGTACGGTGCAGAAATTA | 18357 |
| QY | 841 | AACTCAAAAGGAATTGACGGGGGCCACAAAGCGGTGGAGCATGTGGTTTAATTGCGAAGC | 900 |
| Db | 18358 | AACTCAAAAGGAATTGACGGGGGCCGCCAAGCGGTGGAGCATGTGGTTTAATTGCGAAGC | 18417 |
| QY | 901 | AACGCGCAGAACCTTACCACCCCTTGACAT----GGCAGGACCGCTGGGAGAGATTCAAGCT | 956 |
| Db | 18418 | AACGCGCAGAACCTTACCAGCTCTTGACATTCGGGGTATGGGCATTTGGAGACAGATGCTCT | 18477 |
| QY | 957 | TTCTCGTAAAGACCTTGCACACAGAGTGCTTGCAATGGCTGTCTGCTAGCTCGGTGCTGAGAT | 1016 |
| Db | 18478 | TCAGTTAGGCTGGCCCCCAAGAACAGTGCTGCATGTGGCTGTCTGCTGCGTGGAGAT | 18537 |
| QY | 1017 | GTTCGGTTAAGTCCGGCAACAGACGCGCAACCCAGCTCCCTAGTTGCCAGCAATTCAGTTGG | 1076 |
| Db | 18538 | GTTCGGTTAAGTCCGGCAACAGACGCGCAACCCCTGCCCCCTAGTTGCCAGC-ATTAGTTGG | 18596 |
| QY | 1077 | GAACCTATATGGAACCTCCGATGATTAAGTCG-GAGGAAGGTGTGGATGACGTCAAGTCTCT | 1135 |
| Db | 18597 | GCACCTCAAGGGGACTGCCGGTGATAAGCCGAGAGGAAGTGGGGATGACGTCAAGTCTCT | 18655 |
| QY | 1136 | CATGGGCGCTTACGGGTTGGGCTACACACGTGCTACAAATGGTGGTGACAGTGG----- | 1187 |
| Db | 18657 | CATGGGCGCTTACGGGTTGGGCTACACACGTGCTACAAATGGTGGTGACAGTGGGCGACGAG | 18716 |
| QY | 1188 | -----GTTAATCCCCAAAAGCACTCTCAGTTCCGGATTGCTCTCTCGCAACTCG | 1234 |
| Db | 18717 | ACAGCGATGTCGAGCTAATCTCCAAAAGCCATCTCAGTTCCGGATTGCACTCTGCAACTCG | 18776 |
| QY | 1235 | AGGCGCATGAAGTTGGAATGCGTAGTAATCCGCGAACAGACATGCCCGGTGGAATAGCTTCC | 1294 |

Db 18777 AGTCATGAAGTTGGAATCGGTAGTAATCGCAGATCAGCATGCTGGCGTGAATACGTTCC 18836
Qy 1295 CGGCGCTTGTACACACCGCCCGTACACCATCGGAGTTGGTTCTACCCGACGAGTCCG 1354
Db 18837 CGGCGCTTGTACACACCGCCCGTACACCATCGGAGTTGGTTTACCCGAGGTAGTCCG 18896
Qy 1355 CTAACCTTCGGGGGCGAGCGCCGACCGTAGATCAGGACTGGGGTGAAGTCTGAACA 1414
Db 18897 CTAACCGCAAGAGGAGCGAGCTAACCCAGCGTAGGGTCAGCGACTGGGGTGAAGTCTGAACA 18956
Qy 1476 GGTAGCGTAGGGAACCTCGCGTGGGATCACCTCCCT 1452
Db 18957 GGTAGCGTAGGGAACCTCGCGTGGGATCACCTCCCT 18994

RESULT 10

US-09-726-774-12
; Sequence 12, Application US/09726774
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1466
; TYPE: DNA
; ORGANISM: Bartonella henselae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1466)
; OTHER INFORMATION: n = A,T,C or G
US-09-726-774-12

Query Match 75.3%; Score 1093.6; DB 32; Length 1466;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 1278; Conservative 0; Mismatches 161; Indels 29; Gaps 6;
Qy 8 TCCTGGCTCAGAACGACGCTGGCGGAGGCTTAACACATGCAAGTCGAGCG-AGACCTT 66
Db 1 TCCTGGCTCAGATGACGCTGGCGGAGGCTTAACACATGCAAGTCGAGCGACTATT 60
Qy 67 CGGTCTAGCGCGGAGGCTGAGTAACGCGTGGGAACGTCCTTCTACGGAATAGC 126
Db 61 TAGAGTGAGCGGAGGCTGAGTAACGCGTGGGAATCTACCTTTTCTACGGAATAC 120
Qy 127 CCGGGAACCTGGGAGTAATACCGTATACGCCCTTTGGGGAAGATTTATCGGAGG 186
Db 121 ACAGAGAAATTGTGCTAATACCGTATACGTCCTACTGGGAAAGATTTATCGGAGG 180
Qy 187 ATCGCGCCGCTTGGATTAGTGTGGTGGTAAATGGCCACCAAGCCGACGATCCAT 246
Db 181 ATGAGCCGCTTGGATTAGTGTGGTGGTAAAGGCTCACCAGGCGACGATCCAT 240
Qy 247 AGCTGGTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCGAGACTCCTACGG 306
Db 241 AGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCGAGACTCCTACGG 300
Qy 307 GAGCAGCAGTGGGGAATCTAGACAAATGGGGCAACCCCTGATCAGCCATCGCGCTGA 366
Db 301 GAGCAGCAGTGGGGAATTTGGACAATGGGGCAACCCCTGATCAGCCATCGCGCTGA 360
Qy 367 GTGATGAGGCTTGGGTTGTAAGCTCTTACGCTGGGAGATTAATGACGCTACCGAGC 426
Db 361 GTGATGAGGCTTGGGTTGTAAGCTCTTACGCTGGGAGATTAATGACGCTACCGAGC 420
Qy 427 AGAAGAGCCCGGCTAACTCCGTGCGAGCAGCGCGGTAAATACGAGGGGGCTAGCGTT 486

Db 421 AGAAGAGCCCGGCTAACCTTCGTGCGCAGCAGCGCGGTAAATACGAAGGGGGCTAGCGTT 480
Qy 487 GTTCGGAATTAAGTGGGCTAAAGCGCAGCTAGGCGGACTGGAAGAGTCAGAGGTGAATCC 546
Db 481 GTTCGGAATTAAGTGGGCTAAAGCGCAGCTAGGCGGATATTAAGTCAGAGGTGAATCC 540
Qy 547 CAGGGCTCAACCTTTGGAACTCCCTTTGAACTATCATGCTCGAGTTCGAGAGAGGTGAGT 606
Db 541 CAGGGCTCAACCTTTGGAACTCCCTTTGAACTATCATGCTCGAGTTCGAGAGAGGTGAGT 600
Qy 607 GGAATTCGAGTGTAGAGGTCAAAATTCGTAGATATTCGGAGAACACACAGTGGCGAAGGC 666
Db 601 GGAATTCGAGTGTAGAGGTAAATTCGTAGATATTCGGAGAACACACAGTGGCGAAGGC 660
Qy 667 GGCTCACTGGCTCGATACCTGAGGTGCGAAAGCGTGGGAGCAGCAACAGGATTAGA 726
Db 661 GGCTCACTGGCTCGATACCTGAGGTGCGAAAGCGTGGGAGCAGCAACAGGATTAGA 720
Qy 727 TACCTGTGTAGTCCACGCCGTAAACGATGAATCCAGACGTCGCGAAGCATGCTGTGCG 786
Db 721 TACCTGTGTAGTCCACGCCGTAAACGATGAATGTTAGCCGTTGGGTGTTTACTGCTCAG 780
Qy 787 TGTACACCTAACCGATTAAACGATTCGCCCTGGGAGTACGCTGCCAAGATTAAACATCA 846
Db 781 TGGCGCAGCTAACGATTAACATTCGCCCTGGGAGTACGCTGCCAAGATTAAACATCA 840
Qy 847 AAGGAATTGACGGGGCGCCGACAGCGTGGAGCATGCTGTTTAAATCGAAGCAACCGG 906
Db 841 AAGGAATTGACGGGGCGCCGACAGCGTGGAGCATGCTGTTTAAATCGAAGCAACCGG 900
Qy 907 CAGAACCTTACCAACCTTGACATGGCAGGACCG----CTGGAGAGATTACGTTTCTCG 962
Db 901 CAGAACCTTACCAACCTTGACATGGCAGGAGTGGGAGTGGAGACACCTCTTCAGTT 960
Qy 963 TAAGAGACCTGCACACAGGTGCTGCATGGCTGCTGTCAGCTCGTGTGTCGAGATGTTCCG 1022
Db 961 CGGCTGGATCGGACAGGTGCTGCATGGCTGCTGTCAGCTCGTGTGTCGAGATGTTCCG 1020
Qy 1023 TTAAGTCGGCAACGAGGCGCAACCCAGTCCTAGTTCGACGATTCAGTGGGAATC 1082
Db 1021 TTAAGTCGGCAACGAGGCGCAACCCAGTCCTAGTTCGACG-ATTACGTTGGGCACTC 1079
Qy 1083 TATGAAACTGCCGATGATAAGTCG-GAGGAAGGTGTGATGACGTCAGTCAAGTCTCATGG 1141
Db 1080 TAGGGGACTGCCGCTGATAGCCGAGAGGAGGTGGGATGACGTCAAGTCTCATGGC 1139
Qy 1142 CCTTACGGTTGGGCTACACAGCTGCTACAATGTTGTTGACAGTGG----- 1187
Db 1140 CCTTACGGTTGGGCTACACAGCTGCTACAATGTTGTTGACAGTGGGCGAGATCGCA 1199
Qy 1188 -----GTTAATCCCAAAAGCCATCTCAGTTCGGATTGCTCTGCAACTCGAGGCA 1240
Db 1200 AGTTCGAGCTAATCTCCAAAGCCATCTCAGTTCGGATTGCACTCTGCAACTCGAGTCA 1259
Qy 1241 TGAAGTTGGAATCGCTAGTAAATCGCGAACAGCATCGCGGTGAATACGTTCCCGGGCC 1300
Db 1260 TGAAGTTGGAATCGCTAGTAAATCGTGGATCAGCATGCTACGTTGAATACGTTCCCGGGCC 1319
Qy 1301 TTGTACACACCGCCGCTACACCATGGAGTTGTTTACCCGAGCAGCGTGGCTTACC 1360
Db 1320 TTGTACACACCGCCGCTACACCATGGAGTTGTTTACCCGAGGTCGTGCTGTAACC 1379
Qy 1361 TTCGGGGGAGGCGGCGCAGGTAGGATCAGCGACTGGGTGAAGTCTGAACAAGGTAGC 1420
Db 1380 GCAAGAGGAGGAGGTAAACACGCTAGGTGAGGTACGCGACTGGGGTGAAGTCTGAACAAGGTAGC 1439
Qy 1421 CGTAGGGGAACCTCGCGCTGGATCACCT 1448
Db 1440 CGTA-GGGAACCTCGCGCTGGATCACCT 1466

RESULT 11
PCT-US98-23674-2/c

Best Local Similarity 86.2%; Pred. No. 0; Mismatches 177; Indels 23; Gaps 3;
Matches 1245; Conservative 0;

QY 20 ACAGAGCTGCGGCGAGGCTTAAACACATGCAAGTCGAGCAGACCTTCGGGTCTAGCGG 79
DB 1502 ACAGAGCTGCGGCGAGGCTTAAACACATGCAAGTCGAGCAGACCTTCGGGTCTAGCGG 1443
QY 80 GGAGGGTGAATAACGCTGGGAACGTCCTTCTACGGAATAGCCCGGGAACATGG 139
DB 1442 GGAGGGTGAATAACGCTGGGAACGTCCTTCTACGGAATAGCCCGGGAACATAG 1383
QY 140 GAGTAATACCTATACGCTTGGGGAAGATTTATCGAGAGGATTCGCGCGGCTT 199
DB 1382 GGCTAATACCGATACGCTTATGGGAAGATTTATCGCGGAAGATTCGCGCGGCTT 1323
QY 200 GATTAGTGTGTTGGGGTAAATGGCCCAACGACGATCCATAGCTGGTTGAGA 259
DB 1322 TGATTAGTGTGTTGGGGTAAATGGCCCAACGACGATCCATAGCTGGTTGAGA 1263
QY 260 GATGATCAGCCACTGGGACTGAGACACGCGCCAGACTCCTACGGGAGCAGAGTGG 319
DB 1262 GGATGATCAGCCACTGGGACTGAGACACGCGCCAGACTCCTACGGGAGCAGAGTGG 1203
QY 320 GGAATCTAGACATGGGGCAACCTGATAGCCATGCGCGTGTGATGAGGCT 379
DB 1202 GGAATCTAGACATGGGGCAACCTGATAGCCATGCGCGTGTGATGAGGCT 1143
QY 380 TAGGTTGTAAGCTCTTTCAGCTGGGAAGATTAATGACGGTACGAGCAAGAGACCCCG 439
DB 1142 TAGGTTGTAAGCTCTTTCAGCTGGGAAGATTAATGACGGTACGAGCAAGAGACCCCG 1083
QY 440 GCTAACTCCGTCAGCAGCCGCGTAAATACGGAGGGCTAGCGTTTTCGGAATTA 499
DB 1082 GCTAACTCCGTCAGCAGCCGCGTAAATACGGAGGGCTAGCGTTTTCGGAATTA 1023
QY 500 GGGCTAAAGCCAGCTAGGCGGACTGGAAGTACGAGTGAATCCAGGCTCAACT 559
DB 1022 GGGCTAAAGCCAGCTAGGCGGACTGGAAGTACGAGTGAATCCAGGCTCAACT 963
QY 560 TGGAACTCCCTTTGAACTATCAGTCTGGAGTTCGAGAGAGTGTGATGGAATCCGAGT 619
DB 962 CAGATGCGCTTCGATATCGGACGCTGAGTATGTTAGAGTGTGTTGGAAGTGGAGT 903
QY 620 TAGAGTGAATTCGTAGATATTCGAGAGACACAGTGGCGAAGGGCTCACTGGCT 679
DB 902 TAGAGTGAATTCGTAGATATTCGAGAGACACAGTGGCGAAGGGCTCACTGGCT 843
QY 680 GATAGTACGCTGAGTGGGAGCGTGGGAGCAACAGATTAATACCTGGTAGTC 739
DB 842 ATTACTGACGCTGAGGCGGAAAGCGTGGGAGCAACAGATTAATACCTGGTAGTC 783
QY 740 CAGCGCTAAACGATGAATCCAGACGTCGCAAGCATGCTTTCGGTGTACACACCTAAC 799
DB 782 CAGCGCTAAACGATGAATCCAGACGTCGCAAGCATGCTTTCGGTGTACACACCTAAC 723
QY 800 GATTAAAGCATTCGCGCTGGGAGTACGCTGCGCAAGATTAACCTCAAGGAATTCAGG 859
DB 722 GCTTTGAGCATTCGCGCTGGGAGTACGCTGCGCAAGATTAACCTCAAGGAATTCAGG 663
QY 860 GGGCCCGCACAAGCGGTGGACATGTGTTTAAATTCGAAGCAACGCGCAGAACCTTACA 919
DB 662 GGGCCCGCACAAGCGGTGGACATGTGTTTAAATTCGAAGCAACGCGCAGAACCTTACA 603
QY 920 ACCCTTGATGCGGAGGACCGCTGGAGAGATTCAGCTTTCGTAAGAGACCTGCACACA 979
DB 602 TCCITTGACATGGCGTGTATCCAGAGAGATTTGGGTGCCACTTCGGTGGCGGCACACA 543
QY 980 GGTGCTGATGGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1039
DB 542 GGTGCTGATGGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483
QY 1040 CGCAACCCAGCTCCCTAGTTCGACCAATTCAGTTGGGAATCTATGGAATCTCCGATG 1099

DB 482 CGAACCCACGCTCTTAGTTCCCATC-ATTCAAGTTGGCACTTAGGAGAGACTGCCGGT 424
QY 1100 ATAAGTCG-GAGGAAGGTGTGATGACGTCAAGTCTCATGGGCTTACGGGTGGGCTA 1158
DB 423 ATAAGCCGCGAGGAAGGTGTGATGACGTCAAGTCTCATGGGCTTACGGGTGGGCTA 364
QY 1159 CACAGTGTCTACATGGTGGTGACAGTG------GTTAATCCCC 1197
DB 363 CACAGTGTCTACATGGGCTGACAGTGGGAGCGAAGAGCGATCTCGAGCAATCCCC 304
QY 1198 AAAAGCCATCTCAGTTCGATTGCTCTGCAACTCGAGGCGATGAAGTTGGAATCGCTA 1257
DB 303 AAAAGCCGCTCAGTTCGATTGCTCTGCAACTCGAGTGCATGAAGCGGATCGCTA 244
QY 1258 GTAATCGCGAACAGCATGCGCGGTGAATAGTTTCCCGGCTTGTACACACCGCCGT 1317
DB 243 GTAATCGTGGATCAGCATGCGCGGTGAATAGTTTCCCGGCTTGTACACACCGCCGT 184
QY 1318 CACACCATGGAGTGGTTTACCCGACGACGNTGCGCTAACCTTCGGGGGCGAGCGG 1377
DB 183 CACACCATGGAGTGGTTTACCCGACGCGCTGCGCAACCCGAGGAGCGAGCGAC 124
QY 1378 CACGTTAGGATCAGGACTGGGTCAGTTCGTAACAGGTAGCCGTAGGGAACTGGG 1437
DB 123 CACGTTAGGATCAGGACTGGGTCAGTTCGTAACAGGTAGCCGTAGGGAACTGGG 64
QY 1438 CTGGA 1442
DB 63 CTGGA 59

RESULT 13
US-09-894-467-2/c
; Sequence 2, Application US/09894467
; GENERAL INFORMATION:
; APPLICANT: Lindner, Luther E.
; APPLICANT: MacPhee, Kathleen
; TITLE OF INVENTION: Human Blood Bacterium
; FILE REFERENCE: D6026D
; CURRENT APPLICATION NUMBER: US/09/894,467
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/187,946
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 20
; LENGTH: 1502
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: 58 rRNA sequence of a new human blood bacterium
US-09-894-467-2

Query Match 74.8%; Score 1086.4; DB 37; Length 1502;
Best Local Similarity 86.2%; Pred. No. 0;
Matches 1245; Conservative 0; Mismatches 177; Indels 23; Gaps 3;

QY 20 ACAGAGCTGCGGCGAGGCTTAAACACATGCAAGTCGAGCAGACCTTCGGGTCTAGCGG 79
DB 1502 ACAGAGCTGCGGCGAGGCTTAAACACATGCAAGTCGAGGAGACCTTCGGGTCTAGCGG 1443
QY 80 GGAGGGTGAATAACGCTGGGAACGTCCTTCTACGGAATAGCCCGGGAACATGG 139
DB 1442 GGAGGGTGAATAACGCTGGGAACGTCCTTCTACGGAATAGCCCGGGAACATAG 1383
QY 140 GAGTAATACCTATACGCTTGGGGAAGATTTATCGAGAGGATTCGCGCGGCTT 199
DB 1382 GGCTAATACCGATACGCTTATGGGAAGATTTATCGCGGAAGATTCGCGCGGCTT 1323
QY 200 GATTAGTGTGTTGGGGTAAATGGCCCAACGACGATCCATAGCTGGTTGAGA 259
DB 1322 TGATTAGTGTGTTGGGGTAAATGGCCCAACGACGATCCATAGCTGGTTGAGA 1263
QY 260 GATGATCAGCCACTGGGACTGAGACACGCGCCAGACTCCTACGGGAGCAGAGTGG 319

Db 1262 GGATGATACCCACACTGGGACTGAGACAGCGGCCACACTCTACGGGAGGACGACGTGG 1203
QY 320 GGAATCTTAGACAAATGGGCAACCTGATCTAGCCATGCCGCTGAGTGATCAAGGCCT 379
Db 1202 GGAATATGGACAATGGGCAACCTGATCCAGCCATGCCGCTGAGTGATGAAGCCT 1143
QY 380 TAGGGTGTAAAGCTCTTTTCAGCTGGGAAGATATGACGGTACACAGAGAAGCCCG 439
Db 1142 TAGGGTGTAAAGCTCTTTTCAGGGAGCAATATGACGGTACCGGAGGAATAGCCCG 1083
QY 440 GCTAACTCCGTGACAGCCGCGGTAAATGAGGAGGGGTAGCTGTTTCGGAATACT 499
Db 1082 GCTAACTCTGTCAGCAGCCGCGGTAAATGAGGAGGGGTAGCTGTTTCGGAATACT 1023
QY 500 GGGCGTAAAGCGCAGCTAGCGGACTGGAAGTGCAGAGGTGAATCCACGGGCTCAACCT 559
Db 1022 GGGCGTAAAGCGGCGGTATCGCGGCTTTAAGTCGGGGTGAAGCCGTGCGCTCAACCA 963
QY 560 TGAAGCTCCCTTTGAAACTATCAGTCTGGAGTTCGAGAGGTGAGTGAATCCGAGTG 619
Db 962 CAGAATGGCCTTCGATACTGGGACGCTGAGTATGTTAGAGTGTGGTGAACCTCGAGTG 903
QY 620 TAGAGGTGAATTCGTAGATATTCGAGAGAACACCAAGTGGGAGGCGGCTCACTGGCTC 679
Db 902 TAGAGGTGAATTCGTAGATATTCGCAAGAACACCGGTGGGAGGCGGCAACTGGACC 843
QY 680 GATACGACCTGAGTGGCAAGCGTGGGAGCAACAGGATAGATACCTGGTGTAGTC 739
Db 842 ATTACTGACCTGAGCGCGGAAAGCGTGGGAGCAACAGGATAGATACCTGGTGTAGTC 783
QY 740 CAGCCGTAACGATGAATCCAGAGCGTGGGAGCAATGCTTGTGCGTGTACACCTTAAC 799
Db 782 CAGCCGTAACGATGAATCCAGAGCGTGGGAGCAATGCTTGTGCGTGTACACCTTAAC 723
QY 800 GATTAAAGCAATCCGCTGGGAGTACGCTGCGAAGATTTAAACTCAAAGGAATGACGG 859
Db 722 GCTTGAAGCAATCCGCTGGGAGTACGCTGCGAAGATTTAAACTCAAAGGAATGACGG 663
QY 860 GGGCCGCAACAGCGGTGGAGATGTTGTTAATCGAAGCAAGCGGCAACCTTTACCA 919
Db 662 GGGCCGCAACAGCGGTGGAGATGTTGTTAATCGAAGCAAGCGGCAACCTTTACCA 603
QY 920 ACCTTGCATGTCAGAGACCGCTGGAGAGATTCAGCTTCTCGTAAGAGACCTGCACACA 979
Db 602 TCCTTGCATGTCAGAGATTTACAGAGAGATTTGGGTCCACTTCGGTGGCGGCACACA 543
QY 980 GGTGCTGCATGTCGTGTCAGCTGCTGTCGTCGAGATGTTGCGTTAAGTCCGGCAAGAG 1039
Db 542 GGTGCTGCATGTCGTGTCAGCTGCTGTCGTCGAGATGTTGCGTTAAGTCCGGCAAGAG 483
QY 1040 CGCAACCCAGCTGCTAGTTCGAGCAATTCAGTGGGACTCTATGGAACCTGCCGATG 1099
Db 482 CGCAACCCAGCTGCTAGTTCGAGCAATTCAGTGGGACTCTATGGAACCTGCCGATG 424
QY 1100 ATAAGTCG -GAGGAAGTGTGGATGAGCTCAAGTCCATCGGCTTACGGTGTGGGCTA 1158
Db 423 ATAAGTCGGAAGAGTGTGGATGAGCTCAAGTCCATCGGCTTACGGGATGGGCTA 364
QY 1159 CACAGTGTACAAATGGTGTGACATGG-----GTTAATCCCC 1197
Db 363 CACAGTGTACAAATGGTGTGACATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 304
QY 1198 AAAAGCCATCTAGTTCGATGTCCTGCACTCAGGCGCATGAAGTGGGAATCGCTA 1257
Db 303 AAAAGCCGCTCAGTTCGATGTCCTGCACTCAGGCGCATGAAGTGGGAATCGCTA 244
QY 1258 GTATCCGGAACAGCATCGCGGTGAATACGTTCCCGGCTTGTACACACCGCCCGT 1317
Db 243 GTATCCGGAACAGCATCGCGGTGAATACGTTCCCGGCTTGTACACACCGCCCGT 184
QY 1318 CACACCATGGAGTGTGTTCTTACCCGACGAGTTCGCTAACCTTCGGGGGAGGCGGC 1377

Db 183 CACACCATGGGACTTGGTCTTACCCGACGGCGTGGCCCAACCCGCAAGGAGGAGGCGGAC 124
QY 1378 CAGGTAGGATCAGGACTGGGTGAAGTCTTAACAAGGTAGCCGTAGGGGAACCTGCGG 1437
Db 123 CAGGTAGGTCAGGACTGGGTGAAGTCTTAACAAGGTAGCCGTAGGGGAACCTGCGG 64
QY 1438 CTGGA 1442
Db 63 CTGGA 59
RESULT 14
US-09-900-876-2
; Sequence 2, Application US/09900876
; GENERAL INFORMATION:
; APPLICANT: WATANABE, KATSUJI
; APPLICANT: OKUDA, MITSURU
; TITLE OF INVENTION: METHOD AND SYSTEM FOR SEARCHING FOR RELATIONSHIPS BETWEEN B1
; FILE REFERENCE: 210847USOX
; CURRENT APPLICATION NUMBER: US/09/900,876
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: JP 2000-215134
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1490
; TYPE: DNA
; ORGANISM: Rhodospirillum rubrum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (72)..(73)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (85)..(85)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (485)..(485)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (490)..(490)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (596)..(596)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (709)..(709)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (828)..(828)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (875)..(875)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (910)..(911)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (988)..(988)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (1045)..(1045)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (1332)..(1333)
; OTHER INFORMATION: n = c, g, a, or t
; NAME/KEY: misc_feature
; LOCATION: (1408)..(1408)
; OTHER INFORMATION: n = c, g, a, or t

| | | | |
|--------------------------------------|-----|--|--|
| NAME/KEY: misc feature | | 71.98; Score 1044.6; DB 38; Length 1490; | |
| LOCATION: (1437)..(1442) | | Best Local Similarity 83.98; Pred. No. 6.1e-303; | |
| OTHER INFORMATION: n = c, g, a, or t | | Matches 1941; Conservative 0; Mismatches 208; Indels 31; Gaps 7; | |
| NAME/KEY: misc feature | | | |
| LOCATION: (1451)..(1475) | | | |
| OTHER INFORMATION: n = c, g, a, or t | | | |
| US-09-900-876-2 | | | |
| Qy | 1 | AGTTGATCTCGCTCAGAACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCG- 59 | |
| Db | 11 | AGTTGATCTCGCTCAGAACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCG- 70 | |
| Qy | 60 | -AGACCTTCGGTCTAGCGCGGAGCGGTGAGTAACGCTGGGAAACGTCCTCTCTAC 118 | |
| Db | 71 | ANNCCTTCGGGGTGNAGCGCGGAGCGGTGAGTAACGCTGGGAAACGTCCTCAGGCTCT 130 | |
| Qy | 119 | GGATAGCCCCGGGAACCTGGGAGTAATACCGTATACGCCCTTTGGGGGAAGATTATC 178 | |
| Db | 131 | GGATAGCTCTGGAACGCGACCTATACCGGATACGCCGTATTGGGAAGAAAT--TC 188 | |
| Qy | 179 | GGAGAAGGATCGGCCCGCTTGGATTAGTGTAGTGGGTAAATGGCCCCCACCAGCCGA 238 | |
| Db | 189 | GGCCTTGGATGGGCCCGCTTGGATTAGTGTAGTGGGTAAATGGCCCCCACCAGCCGA 248 | |
| Qy | 239 | CGATCCATAGCTGGTTGAGAGGATGATCAGCACACTGGGACTGAGACAGGCCCCAGAC 298 | |
| Db | 249 | CGATCCATAGCTGGTTGAGAGGATGATCAGCACACTGGGACTGAGACAGGCCCCAGAC 308 | |
| Qy | 299 | TCCTACGGGAGGACGAGTGGGAACTTACAGAACTGGGGCAACCTGATCTAGCCATG 358 | |
| Db | 309 | TCCTACGGGAGGACGAGTGGGAACTTACAGAACTGGGGCAACCTGATCTAGCCATG 368 | |
| Qy | 359 | CCGCGTAGTGATGAAGCCCTTAGGGTTGTAAGCTCTTTACGTGGGAAGATAATGACG 418 | |
| Db | 369 | CCGCGTAGTGATGAAGCCCTTAGGGTTGTAAGCTCTTTACGTGGGAAGATAATGACG 428 | |
| Qy | 419 | GTACCAGCAGAGAGCCCGGCTAAGTCCGTCGCCAGCAGCCGCGGTAAATACGAGGGG 478 | |
| Db | 429 | GTACCTCGAAGAAAGTCCCGGTAAGTCCGTCGCCAGCAGCCGCGGTAAATACGAGGGG 488 | |
| Qy | 479 | CTAGCGTTGTTGCGAATTAAGTGGCGTAAAGCGCAGCTAGCGGAGTGGAAAGTCAGAG 538 | |
| Db | 489 | CNAGCGTTGTTGCGAATTAAGTGGCGTAAAGCGCAGCTAGCGGAGTGGAAAGTCAGAG 548 | |
| Qy | 539 | TGAATCCCGAGGCTCAACTTGGAACTGCTTTGAACATATCAGTCTGGAGTTCGAGAG 598 | |
| Db | 549 | TGAAGCCCGGGCTCAACTTGGAACTGCTTTGAACATATCAGTCTGGAGTTCGAGAG 608 | |
| Qy | 599 | AGGTGAGTGGAAATCCGAGTGTAGAGTGAATTCGTAGATATTCGGAGGAACACCACTG 658 | |
| Db | 609 | AGGTGAGTGGAAATCCGAGTGTAGAGTGAATTCGTAGATATTCGGAGGAACACCACTG 668 | |
| Qy | 659 | GCGAAGCGGCTACTGGCTGATGACCTGAGCTGAGTGGAAAGCGTGGGAGCAACA 718 | |
| Db | 669 | GCGAAGCGGCTACTGGCTGATGACCTGAGCTGAGTGGAAAGCGTGGGAGCAACA 728 | |
| Qy | 719 | GGATTAGATACCTTGGTAGTCCAGCGGTAAACGATGAATCCAGAGCTCGCGCAAGCAT - 777 | |
| Db | 729 | GGATTAGATACCTTGGTAGTCCAGCGGTAAACGATGAATCCAGAGCTCGCGGTCTTA 788 | |
| Qy | 778 | GCTTGTGGGTGCACACCTTAACGATTAAGCATTCGCCCTGGGGAGTACGGTGCAGAGAT 837 | |
| Db | 789 | GAGTTTCGGTATCGACGTAACGCATTAAGCACCCCGCCGCGGGGAGTACGGCCCAAGGT 848 | |
| Qy | 838 | TAAACCTCAAGGAATTAAGCGGGCCCGCACAGCGGTGGAGCATGTGTTTAATTCGA 897 | |
| Db | 849 | TAAACCTCAAGGAATTAAGCGGGCCCGCACAGCGGTGGAGCATGTGTTTAATTCGA 908 | |
| Qy | 898 | AGCAACGCGAGAACCTTACCAACCTTTGACATGGCAGGACCGCTGGAGAGATT - CAGC 955 | |

RESULT 15
US-10-015-127-578
; Sequence 578, Application US/10015127
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Sphingomonas elodea genome sequences and uses thereof
; FILE REFERENCE: 38-10(13806)B
; CURRENT APPLICATION NUMBER: US/10-015,127
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/252,455
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 14357
; SEQ ID NO 578
; LENGTH: 60918
; TYPE: DNA
; ORGANISM: Sphingomonas elodea
US-10-015-127-578

Query Match 71.98; Score 1044.2; DB 44; Length 60918;
Best Local Similarity 84.6%; Pred. No. 3.1e-302;
Matches 1252; Conservative 0; Mismatches 199; Indels 29; Gaps 6;
Qy 1 AGTTGATCTCGCTCAGAACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCGGA 60
Db 16289 AGTTGATCTCGCTCAGAACGCTGGCGCAGGCTTAACACATGCAAGTCGAGCGGA 16348
Qy 61 GA--CCTTCGGGTCTAGCGGCGGAGTGAACCGTGGGAGACGTGCCCTCTCTAC 118
Db 16349 GATCCTTCGGGGTCTAGTGGCGCACGGGTGCGTAACCGTGGGAGTATCGCTTGGGGTTC 16408
Qy 119 GGAATAGCCCCGGGAAATACCGTATACGCCCTTTGGGGGAAGATTATC 178


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Query Match 57.8%; Score 839.4; DB 5; Length 1542;
Best Local Similarity 75.1%; Pred. No. 3.4e-362;
Matches 1150; Conservative 0; Mismatches 302; Indels 80; Gaps 5;

QY 1 AGTTTGATCCTGGCTAGAACGAAACGCTGGCGGCGCTTTAACACATGCAAGTCGAGCGA 60
|||||

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| | | | | | |
|----|------|---------|--------------|--|------|
| Db | 10 | AGTTTGA | TCATGCTCAGAT | TGAACGCTGGCGCAGGCGCTTAACACATGCAAGTCGCAACGG | 69 |
| Qy | 61 | GACC | ----- | -----TTCGGGTCTAGCGCGGACGGGTGAGTAACGCGTGGGA | 102 |
| Db | 70 | TACAGGA | AGAAAGCTTGC | TTCTTGTGTGAGAGTGGCGACGGGTGAGTAATCTCTGGGA | 129 |
| Qy | 103 | ACGTGCC | TTCTCTACGG | ATAACCCCGGAAACTGGGAGTAAATACCGTATACGCCCTTT | 162 |
| Db | 130 | AACTGCT | GTATGAGGGG | ATAACTACTGAGAAACGGTAGCTAATACCGCATACGTCGCA | 189 |
| Qy | 168 | GGCGGA | AAAG | -----TTTATCGGAGAGGATCGGCCGCGTTGGATTAGGT | 208 |
| Db | 190 | AGACCA | AAAGAGGGG | ACCTTCGCGCCTCTTGGCATCGGATGCCCCAGATGGGATTAGCT | 249 |
| Qy | 209 | AGTTGTG | GGGGTAATG | SGCCCAACGACGATCCATAGCTGCTTTGAGAGGATGATCA | 268 |
| Db | 250 | AGTAGTG | GGGTAAACG | CTCACCCTAGCGACGATCCCTAGCTGCTGAGAGGATGACCA | 309 |
| Qy | 269 | GCCACAC | TGGGACTGAG | ACGCGCCAGACTCCTACGGGAGGACGAGTGGGGAATCTTA | 328 |
| Db | 310 | GCCACAC | TGGAAC | TGAGACACGCTCCAGACTCCTACGGGAGCAGCAGTGGGGAATTC | 369 |
| Qy | 329 | GACAATG | GGGGCAAC | CCCTGATCTAGCCATGCCCGGTGATGATGAAGGCTTTAGGTTGT | 398 |
| Db | 370 | CACAATG | GGGCGAAG | CCCTGATGACGCCATGCCCGGTGATGAAGAAAGGCTTCGGGTGT | 429 |
| Qy | 389 | AAAGCTC | TTTCAGCTG | SGGAAGAT-----RATGACGCTACC | 423 |
| Db | 430 | AAAGTAC | TTTACGGGG | AGGAAGGAGTAAAGTTTAATACCTTTGCTCATGTGACGTTACC | 499 |
| Qy | 424 | AGCAGAA | AGACCCCGG | CTAACTCCGTGCCAGCAGCCCGGTAAATACGAGGGGGCTAGC | 483 |
| Db | 490 | CGCAGA | AGAGCACC | GGCTAACTCCGTGCCAGCAGCCCGGTAAATACGAGGGTGCAGC | 549 |
| Qy | 484 | GTTTGTC | GGAATTA | CTGGGCGTAAAGCGCACGTAGCGGACTGGAAAGTCAGAGGTGAAA | 543 |
| Db | 550 | GTTAATC | CGGAATTA | CTGGGCGTAAAGCGCACGCGGTGTTTAAGTCAGATGTGAAA | 609 |
| Qy | 544 | TCCAGGG | CTCAACCTG | GAACCTGGCTTTCGAAACTATCAGTCTGGGATTCGACAGAGGTG | 603 |
| Db | 610 | TCCCGGG | CTCAACCTG | GAACCTGGCTTTCGAAACTATCAGTCTGGGATTCGAGAGGGG | 669 |
| Qy | 604 | AGTGGAA | TTCCGAGT | GTAGAGTGAAATTCGTAGATATTCGGAGGACACCACTGGCGGAA | 663 |
| Db | 670 | GSTAGA | ATTCAGGTG | TAGCGGTGAAATCGGTAGAGATCTGGAGGAATACCGGTGGCGAA | 729 |
| Qy | 564 | GGCGGCT | CACTGGCT | CGATACTGACCGTGAAGTGGGAAAGCGTGGGAGGCAACACAGGATT | 723 |
| Db | 730 | GGCGGCC | CCCCGAC | CAAGACTACGCTCAGGTGCGAAAGCGTGGGAGCAACACAGGATT | 789 |
| Qy | 724 | AGATAC | CTCGTAGT | CCACCGCTAAACGATGAATGCCAGCCTCGGCAAGCATGCTT-C | 782 |
| Db | 790 | AGATAC | CTCGTAGT | CCACCGCTAAACGATGTCGACTTGGAGGTTGTGCCCTTGGAGCG | 849 |
| Qy | 783 | TCGGTGT | CAACCTAA | CGGATTAAGCATTCGCGCTGGGAGTAGCGTTCGCAAGATTAAAA | 842 |
| Db | 850 | TGGCTC | CGGAGCTA | AGCGGTTAAGTCGACCGCTGGGAGTAGCGCCGCAAGGTTAAAA | 909 |
| Qy | 843 | CTCAAG | GAATTAAC | GGGGGCGCGACAGCGGTGAGCAGATGTTGTTTAATTCGAAGCAA | 902 |
| Db | 910 | CTCAAA | TGAATTA | GACGGGGCGCGCAAGCGGTGGAGCATGTGTTTAATTCGATGCAA | 969 |
| Qy | 903 | CGGCGA | AGACCTTAC | CAACCCCTTGACATGCGACGCGCTGGAGAGATTCAGCTTTCTCG | 962 |
| Db | 970 | CGGAGA | AGACCTTAC | CTTGCTTGGACATCCCGGAAGTTTTCAGAGATGAGAATGTGCCT | 1029 |
| Qy | 963 | TAAGAGA | ACCTTGCA | CAGGTGCTGCTGTCAGCTCGCTGCTGAGATGTTCCG | 1022 |
| Db | 1030 | TCGGRA | ACCGTGAG | ACAGGTTGCTGATGGCTGCTCAGCTCGCTGTGTGGAATGTTGG | 1089 |
| Qy | 1023 | TTAAGTC | CGGCAAC | GAGCGCAACCCAGCTCCCTAGTTGCCAGCAATTCAGTTGGGAACTC | 1082 |
| Db | 1090 | TTAAGTC | CGGCAAC | GAGCGCAACCCCTATCTTTGTTGCCAGGGTTCGCGCCGGGAACTC | 1149 |

| | | | |
|----|------|--|------|
| Qy | 1083 | TATGGAAACTGCCGATGATAAGTCGGAGGAAGGTGTGGATGACGTCAAGTCTCATATGGGC | 1142 |
| Db | 1150 | AAAGGAGACTGCCAGTGATAAATCGGAGGAAGCTGGGATGACGTCAAGTCATCATGGCC | 1209 |
| Qy | 1143 | CTTAGCGGGTTGGGTATACACAGTCTCTACAATTGTTGGTGACAGTG----- | 1186 |
| Db | 1210 | CTTAGCACCAGGGCTACACAGTCTCTACAATGGCGCATACAAGAAGAAGCACCTCGCA | 1269 |
| Qy | 1187 | -----GGTTAATCCCCAAAAGCCATCTCAGTTCCGATTCTCCTCTGCAACTCGAGGGCA | 1240 |
| Db | 1270 | GAGAACGGGACCTCATAAAGTCGTCGTAGTCCGGATTGGAGCTGCAACTCGACTCCA | 1329 |
| Qy | 1241 | TGAAGTTGGAAATCGCTAGTAATCGCGGAACAGCATGCCGGGTGAATAGCTTCCC GGCC | 1300 |
| Db | 1330 | TGAAGTCGGAATCGCTAGTAATCGTGGATCAGAATGCCACGGTGAATACGTTCCC GGCC | 1389 |
| Qy | 1301 | TTGTATACACCGCCCGCTCACACCATGGGAGTTTGGTTTTCTACCCGACGACGNTGCCTAACCC | 1360 |
| Db | 1390 | TTGTATACACCGCCCGCTCACACCATGGGAGTTGGTTTCCAAAGAAGTAGSTAGCTTAACC | 1449 |
| Qy | 1361 | TTGGGGGGGAGGGCCCGCAGGTAGGATACAGCAGCTGGGGGTGAAGTCGTAAAGTAGC | 1420 |
| Db | 1450 | TTGGGAGGGCGCTTACCATTGTGATTATCATTGACTGGGGTGAAGTCGTAAAGGTAAAC | 1509 |
| Qy | 1421 | CGTAGGGGAACCTGCGGCTTGGATCACCTCCTT | 1452 |
| Db | 1510 | CGTAGGGGAACCTGCGGTTGGATCACCTCCTT | 1541 |

RESULT 2

```

US-10-465-448-1
; Sequence 1, Application US/10465448
; GENERAL INFORMATION:
; APPLICANT: Hong Kong University of Science and Technology
; TITLE OF INVENTION: ANTI-FOULING COMPOSITION AND METHOD OF PRODUCTION THEREOF
; FILE REFERENCE: 12669-3
; CURRENT APPLICATION NUMBER: US/10/465,448
; CURRENT FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1490
; TYPE: DNA
; ORGANISM: Vibrio proteolyticus or Vibrio alginolyticus
US-10-465-448-1

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[illegible]

Db 491 CCGTACCTAAATCAGAAACCCAGCGCTAACTAGTCCAGCAGCGGTAATACGTAGGT 550
 Qy 477 GCCTAGCGTTTTCGGAATTAATGCGGCTAAAGCCAGCAGTACGCGGACTGGAAGTCAGA 536
 Db 551 GCGAAGCGTTATCCGGAATTAATGCGGCTAAAGCCAGCAGTACGCGGTTTAAAGTCTGA 610
 Qy 537 GGTGAATCCAGGCGCTCAACCTTGAACCTGCTTTGAACATCATAGTCTGAGTTCGAG 596
 Db 611 TGTGAAGCCACGCGCTCAACCTGCTGAGGCTCATTTGGAACCTGGAACCTTGAAGTCAGA 670
 Qy 597 AGAGGTGAGTGAATTCGAGGTGAGGTGAATTCGTPAGATATTCGAGGAACACACAG 656
 Db 671 AGAGGAAGTGAATTCGAGGTGAGGTGAATTCGTPAGATATTCGAGGAACACACAG 730
 Qy 657 TGGCGAAGCGGCTCAGTGGCTGATGAGTGGCTGAGTGGCTGAGTGGCTGAGTGGCTGAG 716
 Db 731 TGGCGAAGCGGCTCAGTGGCTGATGAGTGGCTGAGTGGCTGAGTGGCTGAGTGGCTGAG 790
 Qy 717 CAGGATTAGATACCTGCTGAGTGGCTGAGTGGCTGAGTGGCTGAGTGGCTGAGTGGCTGAG 776
 Db 791 CAGGATTAGATACCTGCTGAGTGGCTGAGTGGCTGAGTGGCTGAGTGGCTGAGTGGCTGAG 850
 Qy 777 T--GCTTGTGCTGCTGACACCTTAACCGGATTAAGCATTCGCGCTGGGAGTACGTCGCA 834
 Db 851 TCCGCGCTTGTGCTGAGTGGCTGAGTGGCTGAGTGGCTGAGTGGCTGAGTGGCTGAGTGGCT 910
 Qy 835 GATTAAACTCAAGGAATTAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 894
 Db 911 GGTGAAACTCAAGGAATTAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 970
 Qy 895 CGAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 954
 Db 971 CGAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1030
 Qy 955 CTTTCTGCT--AAGAGAGCTGACACAGGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1012
 Db 1031 CTTTCTGCT--AAGAGAGCTGACACAGGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1090
 Qy 1013 AGATGCTCGGTTAAGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1072
 Db 1091 AGATGCTCGGTTAAGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1149
 Qy 1073 TTGGGAATCTATGAAGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1132
 Db 1150 TTGGGCACTCTAAGTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1209
 Qy 1133 CTTATGCGGCTTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1188
 Db 1210 CATCATGCGGCTTATGATTTGGGCTTACACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1269
 Qy 1189 -----TTAATCCCAAAAGCCATCTCAGTTCGAGTTCGCTCTCTGCAA 1230
 Db 1270 GAAACCGGAGGTCAAGCAATCCCAATAGTTTCTCAGTTCGAGTTCGCTCTCTGCAA 1329
 Qy 1231 CTCGAGGCGATGAAGTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 1290
 Db 1330 CTCGACTACATGAAGTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 1389
 Qy 1291 TTCGCGGCGCTTGTACACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1350
 Db 1390 TTCGCGGCGCTTGTACACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1449
 Qy 1351 TCGCTAACTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1409
 Db 1450 TGGAGTACCTTTTAGGAGCTAGCCGCTCGAAGTGGGACAAATGATTTGGGTGAAGTCGT 1509
 Qy 1410 ACAAGGTAGCGGTAGGGAACCTCGGCGTGGATCACCTCCCTT 1452
 Db 1510 ACAAGGTAGCGGTAGGGAACCTCGGCGTGGATCACCTCCCTT 1552

US-09-655-378A-159
 ; Sequence 159, Application US/09655378A
 ; GENERAL INFORMATION:
 ; APPLICANT: BROW, MARY ANN D.
 ; LYAMICHEV, VICTOR I.
 ; OLIVE, DAVID M.
 ; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
 ; PATHOGENS
 ; NUMBER OF SEQUENCES: 165
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MEDLEN & CARROLL
 ; STREET: 220 MONTGOMERY STREET, SUITE 2200
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; COUNTRY: UNITED STATES OF AMERICA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/655,378A
 ; FILING DATE: 05-Sep-2000
 ; CLASSIFICATION: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: CARROLL, PETER G.
 ; REGISTRATION NUMBER: 32,837
 ; REFERENCE/DOCKET NUMBER: FORS-01756
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 705-8410
 ; TELEFAX: (415) 397-8338
 ; INFORMATION FOR SEQ ID NO: 159:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1513 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 159:
 US-09-655-378A-159
 Query Match 51.0%; Score 740.2; DB 5; Length 1513;
 Best Local Similarity 73.8%; Pred. No. 4.9e-230;
 Matches 111; Conservative 0; Mismatches 32; Indels 67; Gaps 11;
 Qy 1 AGTTTGATCTGCTGCTCAGAACGAGCGCTGGCGGAGGCTTAACACATCAAGTCGAGCGA 60
 Db 12 AGTTTGATCTGCTGCTCAGAACGAGCGCTGGCGGAGGCTTAACACATCAAGTCGAGCGA 71
 Qy 61 GACCTTCG-----GGTCTACGCGGAGCGGCTGAGTGAACGCGTGGG-AA 103
 Db 72 TGAAGCTTCTAGCTTGTAGAGTGGATTAGTGGCGCAGCGGTGAGTGAAGTATAGTTAA 131
 Qy 104 CGTCCCTTCTCTACGGAATAGCCCGGGAAGTGGGAGTAAATCCGATATAGTACGCTTT- 162
 Db 132 TCTCCCTTACACAAGAGACAAAGTGGGAACGACTGCTATATCTATCTATCTCTCTCT 191
 Qy 163 -----GGGGGAAGATTATCGGAGAAGATCGGCCCGCTTGGATTAGTAG 210
 Db 192 AACACAGTTCAGTAGGGAAGTTTTCGGTGTAGGATGAGACTATATAGTATCAGTAG 251
 Qy 211 TTGTTGGGTAATGGCCCAACCAAGCCGACGATCCATAGCTGTTTGGAGGATGATCAGC 270
 Db 252 TTGTAAGGTAATGGCTTACCAAGGCTATACGCTTAAGTCTGCTGAGAGGATGATCAGT 311
 Qy 271 CACACTGGGACTGAGACACGCGCCAGACTCTACGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 330
 Db 312 CACACTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 371
 Qy 331 CAATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 390
 Db 372 CAATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 431

| | | | |
|----|------|---|------|
| QY | 391 | AGCTCTTTTACGCTGGGAAG-ATTAATGACGGTACACAGCAGAAGAAGCCCCGGCTAACTCCG | 449 |
| DB | 432 | ACTCCTTTTCTTAGGGAAGAATTTCTGACGGTACCTAAAGGAATAAGCACCGCTAACTCCG | 491 |
| QY | 450 | TGCACGACGCGGGTAAATACGAGGGGGCTAGCGTTGTCGGGAATTACTTGGCGGTAAAG | 509 |
| DB | 492 | TGCACGACGCGGGTAAATACGAGGGGTCAAGCGTTACTCGGAATCACTGGGGCGTAAAG | 551 |
| QY | 510 | CGCACGTAGCGGACTGGAAAGTCAGAGGTGAATCCACAGGGCTCAACCTTGGAACTGCC | 569 |
| DB | 552 | GGCGGTAGCGGATTAATCAAGTCTCTTGTGAATCTAATGGCTTAACCATTAACACTGCT | 611 |
| QY | 570 | TTTGAACACTATCAGTCTGGAGTTCGAGAGAGGTGAGTGGAAATCCGAGTGTAGAGGTGAA | 629 |
| DB | 612 | TGGGAACACTATAGTCTTAGAGTAGGAGAGGCGAGATGGAATTTGGTGTGTAGGGGTAAA | 671 |
| QY | 630 | ATTCTGTAGATATTCCGAGGAACACCACTGGCGAAGCGGCTCACTGCTCGATACTGACG | 689 |
| DB | 672 | ATCCGTAGATATCAACCAAGATACCCATTTGGGAAGGCGATCTGCTGGAATCAACTGACG | 731 |
| QY | 690 | CTGAGGTGCGAAAGCGTGGGAGCAACACAGATTAGATACCCCTGGTAGTCCACCGCTAA | 749 |
| DB | 732 | CTAAGGCGCAAGCGTGGGAGCAACACAGGATTAGATACCTGGTAGTCCACGCGCTAA | 791 |
| QY | 750 | ACGATGAATGCCAGACCTCGCAGCAATG-CTTCTCGGTGTCACACACCTTAACGGATTAAAG | 808 |
| DB | 792 | ACGATGTACACTAGTTCTTGGGTGCTAGTCAATCTCAGTAATGCAGTAACGCAATTAAGT | 851 |
| QY | 809 | ATTCCGCTCGGGAGTAGCGGTGCGAAGATTAAAACTCAAGGAATTCAGCGGGGCGCGCA | 868 |
| DB | 852 | GTACCGCTCGGGAGTAGCGTGCACAGATTAAAACTCAAGGAATAGACGGGGACCGCGCA | 911 |
| QY | 869 | CAAGCGTGGAGCATGTGGTTTAATTCGAAGCAACGCGCAGAACCTTTACCAACCTTGAC | 928 |
| DB | 912 | CAAGCGTGGAGCATGTGGTTTAATTCGAAGATACGCGAAGAACCTTTACCTGGGCTTGAT | 971 |
| QY | 929 | ATGCCAGGACCGCTGGAGAT-----TCAGCTTTCTCGTAAGAGACCTGCACACAGGTG | 983 |
| DB | 972 | ATCCTAAGAACCCTTTAGAGATAAGAGGGTGTCTAGCTGTGCTAGA-ACCTTAGAGACAGGTG | 1030 |
| QY | 984 | CTGCATGGCTGTCTGACGTCGTGCTGAGATGTCGGTTAACTCGCGCAACACGAGCGCA | 1043 |
| DB | 1031 | CTGCACGGCTGTCTGACGTCGTGCTGAGATGTTGGTTAACTCCCGCAACGAGCGCA | 1090 |
| QY | 1044 | ACCCAGTCCCTAGTTCCGACGAATTCAGTTGGGAATCTATGGAATACTGCGGATGATAA | 1103 |
| DB | 1091 | ACCCACGATTATTGTTCTTAACGGTTCCGGCGAGCACTCTAAATAGACTGCC-TTCGTAA | 1149 |
| QY | 1104 | GTGGAGGAAGGTGTGATCAGCTCAAGTCTCTATGGCCCTTACGGGTTGGGCTACACAC | 1163 |
| DB | 1150 | GGAGGAGAAGGTGTGACGACGCTCAAGTCAATCATGGCCCTTATGCCCGAGGGCAGCAC | 1209 |
| QY | 1164 | GTGCTACAATGGTGTGACAGTGGGTT-----AATCCCAAAAG | 1202 |
| DB | 1210 | GTGCTACAATGGCATATAGAATGAGACGCAATACCGGAGGTGGAGCAAAATCTATAAAT | 1269 |
| QY | 1203 | CCATCTCAGTTCGGATTGCTCTGCAACTCGAGGGGATGAAGTTGGAATCGCTAGTAAT | 1262 |
| DB | 1270 | ATGTCCAGTTCGGATTGTTCTCTGCAACTCGAGAGCATGAAGCCGGAATGCGTTAGTAAT | 1329 |
| QY | 1263 | CGCGGAACAG-CATGCCCGGTGAATACGTTCCGGGCCCTTGTACACACCGCCGCTACA | 1321 |
| DB | 1330 | CGTAGATCAGCAATGCTACGGTGAATACGTTCCCGGCTGTGTACTCACCGCCGCTACA | 1389 |
| QY | 1322 | CCATGGAGTTGGTTCTACCCGACGACGNTGCGCTAACTTCGGGGGCGCAGGCCGACG | 1381 |
| DB | 1390 | CCATGGAGTTGATTTCTACTCGAAGCGGAATACTAACT-----AGTTACCGTCCACA | 1443 |
| QY | 1382 | GTAGGATCAGGACTGGGGTGAAGTCTACAGAGTACCGGTAGGGGAACCTTCGGGCTGG | 1441 |
| DB | 1444 | GTGAATCAGCACTGGGGTGAAGTCTGAACAGAGTAACGAGTAACGCTAGGAGAACTTCGGTGG | 1503 |

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Qy 1442 ATCACTCTCT 1451
    |||||
Db 1504 ATCACTCTCT 1513

RESULT 6
US-10-367-794A-3052
; Sequence 3052, Application US/10367794A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Streptococcus pneumoniae complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,794A
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 3245
; SOFTWARE: Proprietary
; SEQ ID NO 3052
; LENGTH: 1497
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae complete genome.
; FEATURE:
; LOCATION: (1974242)...(1975739)
; OTHER INFORMATION: Chromosome - 1 Strand - negative ConnectionObjectNumber
US-10-367-794A-3052

Query Match          49.18; Score 713.6; DB 6; Length 1497;
Best Local Similarity 73.9%; Pred. No. 2.1e-221;
Matches 1090; Conservative 0; Mismatches 295; Indels 90; Gaps 11;

Qy 1 AGTTTGATCTGGCTCAGACGACGCTGCGCGGAGGCTTAACACATGCAAGTCGACGGA 60
    |||||
Db 23 AGTTTGATCTGGCTCAGGACGACGCTGCGGGCTGCCTTAATACATGCAAGTAGAACGC 82
    |||||

Qy 61 -----GACCTTCGGGTCTAGCGGCGGACGGGTGAGTAACGCGT-GGGAACG 105
    |||||
Db 83 TGAAGGAGGAGCTTGCTTCTGTGATGTCGACGGGTGAGTAACGCGTAGGTAAACC 142
    |||||

Qy 106 TGCCTTCTCTACGGAATAGCCCGGGAACCTGGGAGTAATACCGTATACGCCCTTTGGG 165
    |||||
Db 143 TGCCTGTGTAGCGGGGATACTATTGGAACGATAGTAAATACCGCATAGAGTAGATGT 202
    |||||

Qy 166 GGAAGATTTATCGGAGAAG-----GATCGGCCCGCGCTTGGATT 204
    |||||
Db 203 TGCATGACATTTGCTTAAAGGTGCATCTGCATCACTACCAGATGGACCTGCGTTGATT 262
    |||||

Qy 205 AGTGTAGTTGGTGGGTAAATGCCCAACCAAGCCGACGATCCATAGCTGGTTGAGAGGATG 264
    |||||
Db 263 AGCTAGTTGGTGGGTAAACGGCTCACCAGGCGACGATACATACGCCGACCTGAGAGGGTG 322
    |||||

Qy 265 ATCAGCCACACTGGGACTGAGACACGCCCGACACTCCTACGGGAGGACAGATGGGGAAT 324
    |||||
Db 323 ATCGGCCACACTGGGACTGAGACACGCCCGACACTCCTACGGGAGGACAGATGGGGAAT 382
    |||||

Qy 325 CTTAGACAATGGGGGCAACCTCTGATCTAGCCATGCCCGTCACTGATGAAGAGCCCTTAGGG 384
    |||||
Db 383 CTTCCGCAATGGACGGAAGTCTGACCGAGCAACGCCCGCTGAGTGAAGAAGGTTTCCGA 442
    |||||

Qy 385 TTGTAAGCTCTTTTCACTCGGGAAGATA-----TGACG 418
    |||||
Db 443 TCGTAAGACTCTGTTGTAAGAGAAGACGAGTGTGAGAGTGGAAGTTACACTGTGACG 502
    |||||

Qy 419 GTACCACGAGAAAGCCCGGCTAACTCCGTGCCACGACCGCGTAAATACGAGGGGG 478
    |||||
Db 503 GTATCTTACCAGAAAGGGACGGCTAACTAGTGTCCAGACGCCGGGTAAATACGTAGTCC 562
    |||||

Qy 479 CTAGCGTGTTCGGAATTACTTGGCGGTAAAGCGCACGCTAGGCGGACTTGGAAAGCTCAGAG 538
    |||||
Db 563 CGAGCGTGTTCGGATTATTGCGCGTAAAGCGAGCGCAGCGGTTAGATTAAGTCTCAAG 622
    |||||

Qy 539 TGAATCCCGAGGCTCAACCTTGAAGCTGCTTTGAAACTATCAGCTCGAGTTCGAGAG 598
    |||||
Db 623 TTAAGGCTGTGGCTTAACCATAGTA-GGGCTTTGGAACCTGTTTAACCTTCGAGTCAAGAG 681
    |||||

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| | | | |
|------|----|--|------|
| 599 | QY | AGGTGAGTGGAAATTCGGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAACACACAGTG | 658 |
| 682 | Db | GGGAGAGTGGAAATTCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTG | 741 |
| 659 | QY | GGGAAGGCGGCTCACTGGCTCATCTAGCTGAGTGGCGGAAAGCGTGGGAGCAACA | 718 |
| 742 | Db | GGGAAGCGGCTCTCTGGCTTGTAACTGACGTGAGGTCGAAAGCGTGGGAGCAACA | 801 |
| 719 | QY | GGATTAGATACCTGGTAGTCACACCGGTAAACGATGAATGCCAGACGTCGGCAAGCATG | 778 |
| 802 | Db | GGATTAGATACCTGGTAGTCACACCGGTAAACGATGAATGCCAGACGTCGGCAAGCATG | 861 |
| 779 | QY | CTTGCTGACACCTAACGGATTAAAGCATTCGCGCTGGGAGTACGGTTCGCAAGA | 836 |
| 862 | Db | CGGGGTTTAGTCCCTAGTACAGGATTAAGCACTCCGCTGGGAGTACGACCCGCAAG | 921 |
| 837 | QY | TTAAAACTCAAAGGAATTGACGGGGCCGCACAAAGCGGTGAGCATGTGTTTAATTCG | 896 |
| 922 | Db | TTGAARCTCAAAGGAATTGACGGGGCCGCACAAAGCGGTGAGCATGTGTTTAATTCG | 981 |
| 897 | QY | AAGCAACGCGCAAGACCTTTACCAACCCCTTTGACATGGC-AGGACCGGTGGAGAGATTCA | 955 |
| 982 | Db | AAGCAACGCGCAAGACCTTTACCAAGCTTTGACATCCCTCTGACCCGCTCTAGAGATAG | 1041 |
| 956 | QY | TTTTCGTGAAGAGACCTGCACACAGGTGCTGCATGGCTGCTGCAGCTCGTCTCGTGAG | 1015 |
| 1042 | Db | TTTTC-CTTCGGGACAGAGTGACAGGTGGTGTGATGGTCTGCAGCTCGTCTCGTGAG | 1100 |
| 1016 | QY | TGTTGGTTAAAGTCGGCAACAGCGCAACCCAGCTCCCTAGTTGGCAGCAATTCAAGTTG | 1075 |
| 1101 | Db | TGTTGGTTAAAGTCGGCAACAGCGCAACCCCTATGTTAGTTGCCATC-ATTAGTTG | 1159 |
| 1076 | QY | GGAACTCTATGGAACCTCCGATGATAAGTCGGAGGAAGGTGTGATGACGTCAAGTCT | 1135 |
| 1160 | Db | GGCACTCTAGCAGAGTCCGGTAAATAAACCGGAGGAAGTGGGATGACGTCAAAATCAT | 1219 |
| 1136 | QY | CATGGCCCTTAGGGTTGGCTTACACACGCTGTACAATGG----- | 1175 |
| 1220 | Db | CATGCCCTTAGCTGGGCTTACACAGCTGTACAAATGGCTGGTTAACAGAGTCCGCAAG | 1279 |
| 1176 | QY | -TGTTGACAGTGGGTTAATCCGCCAAAAGCCA-TCTCAGTTCCGGATTGTCTCTGCAACTC | 1233 |
| 1280 | Db | CCGGTGACGGCAAGCTAATCTCTTAAAGCCAGCTCTCAGTTCCGATTGTAGGCTGCAACTC | 1339 |
| 1234 | QY | GAGGGCATGAAGTTGGAATTCGTAGTAATTCGGGGAACAGCATGCCGCGGTGTAATAGTTTC | 1293 |
| 1340 | Db | GGCTACATGAATTCGGAATTCGTAGTAATTCGGGGATCAGCAGCCGCGGTGTAATAGTTTC | 1399 |
| 1294 | QY | CCGGGCTTGTACACACCCCGGTACACCATGTTGGTTCTACCCGACGACGNTGC | 1353 |
| 1400 | Db | CCGGGCTTGTACACACCCCGGTTCACACAGAGAGTTGTAAACACCCGAGTCGGTGA | 1459 |
| 1354 | QY | GCTAAACCTTCGGGGGCGACGGCGCCACGGTAGGAT | 1388 |
| 1460 | Db | GGTAACCTTAAGGACCGACCCGCCCTAAGGTGGAT | 1494 |

RESULT 7

US-10-367-794A-3053

05 10 307 734A 3053
; Sequence 3053, Application US/10367794A

GENERAL INFORMATION:

APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.

; TITLE OF INVENTION: Streptococcus pneumoniae complete genome.

FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333

; CURRENT APPLICATION NUMBER: US/10/367,794A

; CURRENT FILING DATE: 2003-02-19

; NUMBER OF SEQ ID NOS:

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; SOFTWARE: PROPRIETARY
```

; SEQ ID NO 3053

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; LENGTH: 1497
; TYPE: DNA

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; TYPE: DNA
ORGANISM:

```

; LOCATION: (1974242)...(1975739)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber
US-10-367-794A-3053

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| Query Match | Score 713.6; | DB 6; | Length 1497; |
|----------------------------|--------------|-----------------|--------------|
| Best Local Similarity | 49.1%; | | |
| Pred. No. 2.1e-221; | 73.9%; | | |
| Matches 1090; Conservative | 0; | Mismatches 295; | Indels 90; |

| | | |
|-----|--|-----|
| 1 | AGTTTGATCTCGGCTCAGAACGAACGCTGCGCGCAGCGCTTAAACACATGCAAGTCGACGCA | 60 |
| | | |
| 23 | AGTTTGATCTCGGCTCAGGACGAACGCTGCGCGCGCTGCCTAATACATGCAAGTAGAAGCC | 82 |
| | | |
| 61 | -----GACCTTCGGGCTCTAGCGCGGAGCGGTGAGTAAACGCT--GGGAACG | 105 |
| | | |
| 83 | TGAAGGAGGAGCTTGCTTCTCTGATGAGTTGGCAACGGGTGAGTAAACGCTAGGTAAACC | 142 |
| | | |
| 106 | TGCCCTTCTCTACGGAATAGCCCGGGAACACTGGGAGTATACCGTATACGCCCTTTGGG | 165 |
| | | |
| 143 | TGCCTGTAGCGGGGATAACTATTGGAAACGATAGCTAATACCGCATAAAGAGTAGATGT | 202 |
| | | |
| 166 | GGAAAGATTATCGGAGAAG-----GATCGGCGCGCGTTGGATT | 204 |
| | | |
| 203 | TGCATGACATTTGCTTTAAAGGTGCATCTTCATCACTACCAGATGGACCTTGCGTTGATT | 262 |
| | | |
| 205 | AGGTAGTTGGTGGGTAATGGCCCAACCAACGACGATCCATAGCTGTTTGAAGAGGATG | 264 |
| | | |
| 263 | AGCTAGTTGGTGGGTAAACGGCTCACCAGGCGACGATACATAGCCGACTGAGAGGGTG | 322 |
| | | |
| 265 | ATCAGCCACACTGGGACTGAGACACGCGCCAGACTCCTACGGGAGCAGCAGTGGGAAT | 324 |
| | | |
| 323 | ATCGCCACACTGGGACTGAGACACGCGCCAGACTCCTACGGGAGCAGCAGTAGGGAAT | 382 |
| | | |
| 325 | CTTAGCAATGGGGCAACCCGTGATCTAGCCATGCCCGTGAGTGATGAAGGCCCTTAGG | 384 |
| | | |
| 383 | CTTCGGCAATGGACGGAAGTGTGACCGAGCAACGCCGCTGAGTGAAGAAGGTTTTCGA | 442 |
| | | |
| 385 | TGTAAAGCTCTTTCAGCTGGGAAGATA-----TGACG | 418 |
| | | |
| 443 | TGTPAAAGCTCTGTTGTAAAGAAAGACGAGTGTGAGATGGAAAGTTCACACTGTGACG | 502 |
| | | |
| 419 | GTACAGCAGAAAGACCCCGGCTAACTCCGTGCCAGCACGCCGCGTAAATACGAGGGGG | 478 |
| | | |
| 503 | GTATCTTACCAGAAAGGACGGCTAACTACGTGCCAGCACGCCGCGTAAATACGTAGTCC | 562 |
| | | |
| 479 | CTAGCGTTGTTCCGAATTACTGGCGGTAAAGCGCACGTAGGCGGACTGGAAGCTCAGAG | 538 |
| | | |
| 563 | CGAGCTTTGTCGGATTATTATGGCGTAAAGCAGCGACGCGGTTAGATAAGTCTGAAG | 622 |
| | | |
| 539 | TGAATCCCGGGCTCAACCTTGGAAGCTGCTTTGAAACTATCAGTCTGGAGTCTCAGAG | 598 |
| | | |
| 623 | TTAAAGGCTGTGGCTTAAACCATGTA--GGCTTTGGAAACGTGTTAACTTGAAGTCCAAG | 681 |
| | | |
| 599 | AGGTGAGTGGAAATCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAGGAACACCAAGT | 658 |
| | | |
| 682 | GGGAGAGTGAATTCCTATGTAGCGGTGAAATCGGTAGATATATGGAGGAACACCGGTG | 741 |
| | | |
| 659 | CGGAAGCGGCTCACTGGCTCGATACGTAGCGCTGAGGTGCGAAAGCGTGGGAGCAAAAC | 718 |
| | | |
| 742 | CGGAAGCGGCTCTCTGGCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGAGCAAAAC | 801 |
| | | |
| 719 | GGATTAGATACCCCTGGTAGTCCACGCGGTAAACGATGAATGCACAGCTCGCGCAAGCATG | 778 |
| | | |
| 802 | GGATTAGATACCCCTGGTAGTCCACGCTGTAAACGATGAGTGTCTAGGTGTAGNACCCCTTC | 861 |
| | | |
| 779 | CTTG--TCGGTGTCAACACCTAACCGATTAAACGATTCGCGCTGGGAGTAGTACGGTCCAAG | 836 |
| | | |
| 862 | CGGGGTTAGTGCCTAGCTAACGCATTAAAGCATCTCGGCTGGGAGTAGACCGCCGAAG | 921 |
| | | |
| 837 | TTAAACATCAAGGAATTGACGGGGGCCCCACAGCGGTGGAGCATGTGGTTTAATTCG | 896 |
| | | |
| 922 | TTGAAACTCAAGGAATTGACGGGGGCCCCACAGCGGTGGAGCATGTGGTTTAATTCG | 981 |
| | | |
| 897 | RAGCAACGCGCAGAACCTTACCAACCCCTTGACATGGC--AGGACCGCTGGAGAGATTACG | 955 |

QY 161 -----CACCTTCGGTCTAGCGCGACGGGTGAGTAACGCT- GGAAGC 105
DB 272 TGAAGGAGAGCTTCTCTCTGATGATGATGCGAAGCGGTGAGTAACGCTGAGTAAC 331
QY 106 TGCCCTTCTACGAATAGCCCGGAACTGGGAGTAATACCGTATATACGCCCTTTGGG 165
DB 332 TGCCCTGAGCGGGGATAACTATTGGAAAGATAGCTAATACCGCATAGAGTAGATGT 391
QY 166 GGAAGATTATTCGAGAGAG-----GATCGCCCGCGGTGGATT 204
DB 332 TGCAATGACATTGCTTTAAAGGTGCACTTGCATCACTACCAAGATGACCTGCTGTATT 451
QY 205 AGGTAGTTGGTGGGTAATGCCCCACCAAGCGAGATCCATAGCTGTTTTCAGAGGATG 264
DB 452 AGCTAGTTGGTGGGTAACGGCTACCAAGGCGAGATACATAGCGACCTGAGAGGTTG 511
QY 265 ATCAGCCACACTGGGACTGAGACAGCGCCGACACTCTACGGGAGGCGACGAGTGGGA 324
DB 512 ATCGCCACACTGGGACTGAGACAGCGCCGACACTCTACGGGAGGCGACGAGTGGGA 571
QY 325 CTTAGCAATAGGGGCAACCTGATCTAGCCATGCGCGGTGATGATGAAGCCCTTAGG 384
DB 572 CTTAGCAATAGGGGCAACCTGATCTAGCCATGCGCGGTGATGATGAAGCCCTTAGG 631
QY 385 TTGTAAGCTCTTTCAGCTGGGAAGATA-----TGAGC 418
DB 632 TCGTAAGCTCTTTCAGCTGGGAAGATA-----TGAGC 691
QY 419 TPACAGCAGAGAAAGCCCGCTAACTCCGTCGACGAGCGCGGTATATACGGAGGG 478
DB 692 GTATCTTACCAGAAAGGAGGCTAACTACGTGCGCAGCGCGGTATATACGGAGGG 751
QY 479 CTAGCGTTGTCGGAATTAAGCGGCTAAGCGGCTAGGCGGCTAGGAAAGTACAGAG 538
DB 752 CGAGCGTTGTCGGAATTAAGCGGCTAAGCGGCTAGGCGGCTAGGAAAGTACAGAG 811
QY 539 TGAATCCAGGCTCAACCTTGAAGTCCCTTTGAACTATCAGTCTGAGTTCGAGAG 598
DB 812 TTAAGGCTGTGGCTTACCATAGTA- GCTTTGAACTGTTTAACTTGAAGTCAAGAG 870
QY 599 AGGTGAGTGGAAATCCGAGTGTAGAGTGAATTCGTAGATATTCGGGAGAACACAGTG 658
DB 871 GGGAGAGTGGAAATCCGAGTGTAGAGTGAATTCGTAGATATTCGGGAGAACACAGTG 930
QY 659 GGGAGAGGCTCACTGGCTGATACGTAGCTGAGTGTGGAAGCGGTGGGAGCAACA 718
DB 931 GCGAAGGCGCTCTCTGGCTTGAATGAGCTGAGGCTGAGGCTGAGGAGCAACA 990
QY 719 GGATTAGATACCTGTAGTCCACCGCTTAACGATGATGCGACAGCTGCGCAAGCATG 778
DB 991 GGATTAGATACCTGTAGTCCACCGCTTAACGATGATGCGACAGCTGCGCAAGCATG 1050
QY 779 CTTG--TCGGTGTACACCTAACGATTAAGCATTCGCGCTGGGAGTACGCTGCAAGA 836
DB 1051 CGGGTTTGTAGTCCGCTAGTACGATTAAGCATTCGCGCTGGGAGTACGCTGCAAGA 1110
QY 837 TTAACCTCAAGGAATTAAGCGGCGCGCAAGCGGTGGAGATGTGTTTTAATTCG 896
DB 1111 TTGAACCTCAAGGAATTAAGCGGCGCGCAAGCGGTGGAGATGTGTTTTAATTCG 1170
QY 897 AAGCAAGCGGAGAACCTTACCAACCTTGCATGCG- AGGACCGCTGAGAGATTCAGC 955
DB 1171 AAGCAAGCGGAGAACCTTACCAACCTTGCATGCG- AGGACCGCTGAGAGATTCAGC 1230
QY 956 TTTTCGTAAGAGACCTGACACAGGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 1015
DB 1231 TTTTC-CTTCGGGAGAGAGTGTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1289
QY 1016 TGTTCGGTTAAGTCCGGCAAGAGCGCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1075
DB 1290 TGTTCGGTTAAGTCCGGCAAGAGCGCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1348

QY 1076 GGAACCTATGAAACTGCCGATGATAAGTCGAGGAGGTGTGATGACGTCAAGTCT 1135
DB 1349 GGCATCTAGCAGACTGCCGTATTAACCGGAGGAGTGGGATGACGTCAATCAT 1408
QY 1136 CATGGCCCTTACGGTTGGGCTACACAGCTGTACAATGG----- 1175
DB 1409 CATGGCCCTTATGACCTGGGCTACACAGCTGTACAATGGCTGTGTTGTTGTTG 1468
QY 1176 TGGTACAGTGGGTTAATCCCAAGGCA-TCACAGTTCGATTGTCTGCAACTC 1233
DB 1469 CCGGTGACGGCAAGCTAATCTTAAAGCCAGTCTCAGTTCGGATTGTAGGCTGCAACTC 1528
QY 1234 GAGGCGATGAAGTTGGAATCGCTAGTAATCGGGGAAACACATGCCCGGTGAATAGCTTC 1293
DB 1529 GCCTACATGAAGTTCGATCGCTAGTAATCGGGGATCAGACGCCGCGGTGAATAGCTTC 1588
QY 1294 CCGGCGCTTGTACACACGCCCGCTCACACATGGGAGTGTCTTACCAGACAGCTGTC 1353
DB 1589 CCGGCGCTTGTACACACGCCCGCTCACACAGAGAGTGTGTAACACCCGAGTCGTGA 1648
QY 1354 GCTAACCTTCGGGGGCGAGCGCCACGCTGAGAT 1388
DB 1649 GGTAAACCGTAAGGAGCCAGCCGCTAAGGTGGAT 1683

RESULT 12
US-10-367-794A-2995
; Sequence 2995, Application US/10367794A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Streptococcus pneumoniae complete genome.
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,794A
; NUMBER OF SEQ ID NOS: 3245
; SOFTWARE: Proprietary
; SEQ ID NO 2995
; LENGTH: 1686
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae complete genome.
; FEATURE:
; LOCATION: (1912227)...(1913912)
; OTHER INFORMATION: Chromosome - 1 Strand - negative ConnectonObjectNumber
US-10-367-794A-2995

Query Match 49.1%; Score 713.6; DB 6; Length 1686;
Best Local Similarity 73.9%; Pred. No. 2.2e-221;
Matches 1090; Conservative 0; Mismatches 295; Indels 90; Gaps 11;
QY 1 AGTTTGTATCTGGCTCAGAACGACGCTGCGGCGAGGCTTAACACATGCAAGTCGAGCA 60
DB 212 AGTTTGTATCTGGCTCAGAACGACGCTGCGGCGAGGCTTAACATGCAAGTCGAGCA 271
QY 61 -----GACCTTCGGGTCTAGCGCGGAGCGGTGAGTAACGCT- GGAAGC 105
DB 272 TGAAGGAGGAGCTTCTCTCTGATGATGTTGCGAAGCGGTGAGTAACGCTGAGTAAC 331
QY 106 TGCCCTTCTCTACGAATAGCCCGGAACTGGGAGTAAATACCGTATACGCCCTTTGGG 165
DB 332 TGCCCTTCTCTACGAATAGCCCGGAACTGGGAGTAAATACCGTATACGCCCTTTGGG 391
QY 166 GGAAGATTATTCGAGAGAG-----GATCGCCCGCGGTGGATT 204
DB 392 TGCAATGACATTGCTTTAAAGGTGCACTTGCATCACTACCAAGATGACCTGCTGTATT 451
QY 205 AGGTAGTTGGTGGGTAATGCGCCCAAGCGAGATCCATAGCTGTTTTCAGAGGATG 264
DB 452 AGCTAGTTGGTGGGTAACGGCTCACCAAGGCGAGATACATAGCGACCTGAGAGGTTG 511
QY 265 ATCAGCCACACTGGGACTGAGACAGCGCCGACACTCTTACCAGAGGCGACGAGTGGGA 324
DB 512 ATCGCCACACTGGGACTGAGACAGCGCCGACACTCTTACCAGAGGCGACGAGTGGGA 571

| | | |
|------|--|------|
| 325 | CTTAGACAATGGGGGCAACCCCTGATCTAGCCATGCGCGTGTAGTGTAGTGAAGGCGCTTAGGG | 384 |
| QY | | |
| Db | | |
| 572 | CTTCGGCAATGGAGCGAAAGTCTGACCGGAGCAACGCCGCTGAGTGAAGAAGGTTTTCCGA | 631 |
| QY | | |
| Db | | |
| 385 | TTGTAAAGCTCTTCAGCTGGGAATAA-----TGACG | 418 |
| QY | | |
| Db | | |
| 632 | TCGTAAAGCTCTGTGTTAGAGAAGAACAAGTGTGAGATGGAAAGTTCACTGTGTGACG | 691 |
| QY | | |
| Db | | |
| 419 | GTACCAAGCAGAAGACCCCGGCTAACTCCGTGCCAGCAGCCGCGTAAATACGGAGGGG | 478 |
| QY | | |
| Db | | |
| 692 | GTATCTTACAGAAAGGACGGCTAACTACGTGCCAGCAGCGCGGTAACTAGTAGTCC | 751 |
| QY | | |
| Db | | |
| 479 | CTAGCGTTGTTCGGAATTACTGGCGCTAAAGCGCACGTAGGGGACGTGGAAGTCAAGAG | 538 |
| QY | | |
| Db | | |
| 752 | CGAGCGTTGTCCGGATTTATTGGCGCTAAAGCGCAGCGCGGTAGATTAAGTCTGAAG | 811 |
| QY | | |
| Db | | |
| 539 | TGAATCCCAAGGCTCAACCTTGGAACTGCCCTTTGAAACTATCACTCTCGAGTTCAGAG | 598 |
| QY | | |
| Db | | |
| 812 | TTAAAGGCTGTGCTTTAACCATAGTA--GGCTTTGGAAACTGTTAACTTGTAGTGCAGAG | 870 |
| QY | | |
| Db | | |
| 599 | AGGTGAGTGGAAATTCGGAGGTAGAGGTGAAATTCGTAGATATTCGGAGGAAACACCAAGT | 658 |
| QY | | |
| Db | | |
| 871 | GGGAGAGTGGAAATTCATGTGTAGCGGTGAAATGCGGTAGATATATCGAGGAACACCGGT | 930 |
| QY | | |
| Db | | |
| 659 | GCAGAGCGGCTCACTGGCTGCATCTAGCTGTAGGTGCGAAAGCGTGGGGAGCAAAACA | 718 |
| QY | | |
| Db | | |
| 931 | GCAGAAAGCGGCTCTCTGGCTTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAAACA | 990 |
| QY | | |
| Db | | |
| 719 | GGATTAGATACCTTGTTAGTCCACGCGGTAAAGCATGAATGCCAGACGTCGGCAACGATG | 778 |
| QY | | |
| Db | | |
| 991 | GGATTAGATACCTTGTTAGTCCACGCTGTAAGCGATGAGTGTAGTGTGTAGACCCCTTTC | 1050 |
| QY | | |
| Db | | |
| 779 | CTTG--TCGGTGTCAACCTCAACGGATTAAGCATTCGCGCTGGGGAGTAGCGGTCGCAAGA | 836 |
| QY | | |
| Db | | |
| 1051 | CGGGGTTAGTGGCTAGCTTAACGCATTAAGCACTCGCGCTGGGGAGTAGCGACCGCAAG | 1110 |
| QY | | |
| Db | | |
| 837 | TTAAAACTCAAGGAATTAAGCGGGGCGGCACAAAGCGGTGGAGCATGTGGTTAAATCG | 896 |
| QY | | |
| Db | | |
| 1111 | TTGAAACTCAAGGAATTAAGCGGGGCGGCACAAAGCGGTGGAGCATGTGGTTAAATCG | 1170 |
| QY | | |
| Db | | |
| 897 | AAGCAAGCGCAGAACCTTACCAACCCCTTGACATGCG--AGGACCGTGGAGAGATTACAGC | 955 |
| QY | | |
| Db | | |
| 1171 | AAGCAAGCGCAAGAACCTTACCAGGTCTTGACATCCCTCTGACCGGTCTAGAGATAGAGC | 1230 |
| QY | | |
| Db | | |
| 956 | TTTCTCGTAGAGACCTGCACACAGGTGTGTCATGGCTGCTGCTGAGTCGTGCTGTGAGA | 1015 |
| QY | | |
| Db | | |
| 1231 | TTTC-CTTCGGACAGAGGTGCACAGGTGGTGATGTTGTCGTGCTGCTGTGCTGTGAGA | 1289 |
| QY | | |
| Db | | |
| 1016 | TGTTCTGGTTAAGTCCGGCAACAGAGCGAACCACGTCCTTAGTTGCCAGAAATTCAGTTG | 1075 |
| QY | | |
| Db | | |
| 1290 | TGTTGGGTTAAGTCCCGCAACAGAGCGCAACCCCTATTGTTAGTTGGCATC-AATTAGTTG | 1348 |
| QY | | |
| Db | | |
| 1076 | GGAACTCATGGAACCTCCGATGATAAGTTCGAGGAGGAGGTGGATGAGCTCAAGTCCT | 1135 |
| QY | | |
| Db | | |
| 1349 | GGCACTCTACGGAGACTCCGGTAAATAACCGGAGGAAGGTGGGATGAGCTCAAAATCAT | 1408 |
| QY | | |
| Db | | |
| 1136 | CATGGGCTTACCGGTTGGGCTACACAGCTGCTACAAATG-----1175 | |
| QY | | |
| Db | | |
| 1409 | CATGCCCTTATGACCTGGGCTACACAGCTGCTACAAATGCGTGGTACACAGAGTCGAAG | 1468 |
| QY | | |
| Db | | |
| 1176 | -TGGTGACAGTGGGTTAATCCCAAAAGCCA-TCTCAGTTTCGGATGTCTCTGCAACTC | 1233 |
| QY | | |
| Db | | |
| 1469 | CCGCTGACGCAAGCTAATCTTTAAGGCCAGTCTCAGTTCCGATTTAGGCTGCAACTC | 1528 |
| QY | | |
| Db | | |
| 1234 | GAGGGCATGAATTGGATCGCTAGTAATTCGGGAACAGCATGCCCGGTTGAATACGTTTC | 1293 |
| QY | | |
| Db | | |
| 1529 | GCCTACATGAAGTCGGAATCGCTAGTAATTCGCGGATCAGCACCGCGGTTGAATACGTTTC | 1588 |
| QY | | |
| Db | | |
| 1294 | CCGGCCCTTGTACACACCGCGCTCACCATGGAGTTGGTCTACCCGACGACGAGTGC | 1353 |
| QY | | |
| Db | | |
| 1589 | CCGGCCCTTGTACACACCGCGCTCACCATGGAGTTGGTCTACCCGACGACGAGTGC | 1648 |
| QY | | |
| Db | | |
| 1354 | GCTAACCTTCGGGGGCGAGCGGCCAGCGTAGGAT | 1388 |
| QY | | |
| Db | | |

1649 GGTAACCGTAAGGAGCCAGCCGCTAAGTGGGAT 1683

RESULT 13

```

US-10-461-990-1
; Sequence 1, Application US/10461990
; GENERAL INFORMATION:
; APPLICANT: Nestec, S.A.
; APPLICANT: Neeser, Jean-Richard
; APPLICANT: Mollete, B.
; APPLICANT: Stinglele, Francesca
; APPLICANT: Zinc, Robert
; APPLICANT: Kratky, Zoe
; TITLE OF INVENTION: Lactic Acid Bacteria Producing Polysaccharide Similar to those
; FILE OF INVENTION: Human Milk and Corresponding Genes
; FILE REFERENCE: 88265-10322
; CURRENT APPLICATION NUMBER: US/10/461,990
; CURRENT FILING DATE: 2003-06-15
; PRIOR APPLICATION NUMBER: US 09/548,606
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: PCT/EP 98 06636
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: CH 94 203245.2
; PRIOR FILING DATE: 2000-01-01
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: Streptococcus macedonicus
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1460)..(1460)
; OTHER INFORMATION: n is a, c, g, or t
US-10-461-990-1

```

| | | | | | | | |
|----------------------------|--------|--|---------------|--------|-----|--------|-------|
| Query Match | 48.2% | Score | 699.4; | DB | 6; | Length | 1522; |
| Best Local Similarity | 72.8%; | Pred. | No. 8.3e-217; | | | | |
| Matches 1103; Conservative | 0; | Mismatches | 318; | Indels | 94; | Gaps | 12; |
| Qy | 1 | AGTTTGATCCTGGCTCAGACGACGCTGGCGCGAGGCTTAACACATGCAAGTCGAGCGA | 60 | | | | |
| Db | 9 | AGTTCGATCCTGGCTCAGGACGACGCTGGCGCGCTGCCTAATACATGCAAGTAGAACGC | 68 | | | | |
| Qy | 61 | GACCTTCG-----GGTCTACGGCGGACGGGTGAGTACCGCTGGG-NA | 103 | | | | |
| Db | 69 | TGAAGACTTTAGCTTGTAGAGTGTGGAAGAGTTGCCGAACGGGTGAGTACCGGTAGGTA | 128 | | | | |
| Qy | 104 | CGTGCCCTTCTACGGAATAGCCCGGGAACCTGGGAGTAATAACCGTATAC----- | 155 | | | | |
| Db | 129 | CCTGCTTATAGTGGGGGATAACTATTGGAAACGATAGCTAATACCCGATATAGTGTGT | 188 | | | | |
| Qy | 156 | -----GCCCTTTGGGGGAAGATTATCGGAGAAGGATCGGCCCGCTTGA | 202 | | | | |
| Db | 189 | AACACATGTTAGAGACTTTAAAGATGCAATTGCATCTAGTAGTGGACCTGCGTGTGA | 248 | | | | |
| Qy | 203 | TTAGCTAGTTGGTGGGCTAATGGCCACCAAGCCGACGATCCATAGCTGTTTGAAGGA | 262 | | | | |
| Db | 249 | TTAGCTAGTTGGTGGGCTAACGCCCTACCAAGCGGACGATACATAGCCGACCTGACAGG | 308 | | | | |
| Qy | 263 | TGATCAGCCACATGGGAGCTGAGACAGCGGCCAGACTCTACGGGAGGACGAGTGGGA | 322 | | | | |
| Db | 309 | TGATCGGCCACACTGGGACTGAGACACGGCCGACACTCTACGGGAGGACGAGTAGGGA | 368 | | | | |
| Qy | 323 | ATCTTAGACATATGGGGCAACCCCTGATCTAGCCATGCCGCTGAGTGATGAAGGCCCTTAG | 382 | | | | |
| Db | 369 | ATCTTCGCAATGGGGCAA-CTTGACCGAGCAACGCCGCTGAGTGAAGAAAGTTTCG | 427 | | | | |
| Qy | 383 | GGTTGTAAAGCTCTTTTCAGCTGGGAAG-----ATAATGA | 416 | | | | |
| Db | 428 | GATCGTAAAGCTCTGTTGTGAAGAGAACAAGCTGTGTGAGAGTGGAAAGTTTCACACAGTGA | 487 | | | | |

417 CGGTACAGCAGAGAGAGCCCGCGCTAACTCGTCCAGCAGCCCGGTAAATACGAGGG 476
 488 CGGTAACCTACAGAGAGAGCCCGCTAACTAGTCCAGCAGCCCGGTAAATACGAGGT 547
 477 GCCTAGCGCTTGTTCGGATTAATCTGGCGGTAAAGCCAGCAGTGGCGGACTGGAAAGTCAGA- 536
 548 CCCAGAGCGCTTGTTCGGATTAATCTGGCGGTAAAGCCAGCAGTGGCGGACTGGAAAGTCAGA 607
 537 GGTGAATCCAGAGCGCTCAACCTTGGAACTGCTTGAACCTATCATGCTGTGGAGTCCGAG 596
 608 AGTTAAAGCAGCAGTGCCTTAAACCATGTTTC-GCTTTGGAACCTGTTAAACCTTCAGTCGAGA 666
 597 AGAGGTAGTGAATTCGAGGTGTAGAGTGAAGTGAATTCGTAGATATTCGAGAGAACACACAG 656
 667 AGGGAGAGTGAATTCGAGGTGTAGAGTGAAGTGAATTCGTAGATATTCGAGAGAACACACAG 726
 657 TGGCAAGCGCGCTCACTGGCTCGATACCTAGCCTGAGGTGCGAAAGCGTGGGAGCAAA 716
 727 TGGCAAGCGCGCTCACTGGCTCGATACCTAGCCTGAGGTGCGAAAGCGTGGGAGCAAA 786
 717 CAGGATTAGATACCTTGGTGTAGTCCAGCGGTAAAGCATGAATGCCAGACGCTCGGCAAGCA 776
 787 CAGGATTAGATACCTTGGTGTAGTCCAGCGGTAAAGCATGAATGCCAGACGCTCGGCAAGCA 846
 777 TGCCTG--TCGGTGTACACCTAACGGAATTAAGCATTCGCGCTGGGAGTACGCTCGCAA 834
 847 TCCGGGCTTGTTCGGATTAATCTGGCGGTAAAGCCAGCAGTGGCGGACTGGAAAGTCAGA 906
 835 GATTAAACTCAAGGAATTTACGGGGGCGCCGACACAGCGGTGGAGCATGTGTTAAAT 894
 907 GGTGAAACTCAAGGAATTTACGGGGGCGCCGACACAGCGGTGGAGCATGTGTTAAAT 965
 895 CCAAGCAGCGCAGAGACCTTACCAACCTTGACATGCGAGGAGCCGCTGGAGAGATTCAG 954
 966 CCAAGCAGCGCAGAGACCTTACCAACCTTGACATGCGAGGAGCCGCTGGAGAGATTCAG 1024
 955 CTTTCTCGTGAAGAGACCTCGACACAGGTGCTGCATGGCTGCTGCTAGCTGCTGCTGAG 1014
 1025 AAGTTTCTTCGGAACATCGGTGACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAG 1084
 1015 ATGTTTCGTTAAGTCCGGCAAGAGCGCAACCCAGCTCCCTAGTTCGCCAGCAATTCAGTT 1074
 1085 ATGTTTCGTTAAGTCCGGCAAGAGCGCAACCCAGCTCCCTAGTTCGCCAGCAATTCAGTT 1143
 1075 GGAACCTCTATGGAATCCGATGATAAGTTCGAGGAGAGGTGATGACGTCAGTCC 1134
 1144 GGCACCTCTATGGAATCCGATGATAAGTTCGAGGAGAGGTGATGACGTCAGTCC 1203
 1135 TCATGGCCCTTACGGGTTGGGCTTACACAGTGTGCTACAAATGGTGGTGCAGTGGGT 1189
 1204 TCATGGCCCTTATGACCTGGGCTTACACAGTGTGCTACAAATGGTGGTGCAGTGGGT 1263
 1190 -----TAAATCCCAAGAGCCTATCAGTTCGGATGTTGCTGCAACT 1232
 1264 GCGGTGAGCGCAAGCAATTCCTTAAAGCCAACTCAGTTCGGATGTTGCTGCAACT 1323
 1233 CGAGGCGCATGAAGTTGGAATCGCTAGTAAATCGGGAACAGCATCGCGCGGTGATAGTGT 1292
 1324 CGGCTACATGAAGTCGGATCGCTAGTAAATCGGGAACAGCATCGCGCGGTGATAGTGT 1383
 1293 CCGGGCCCTTGTACACAGCGCGCTCACACATGAGTGGAGTGGTTCACCGCAGCAGNTG 1352
 1384 CCGGGCCCTTGTACACAGCGCGCTCACACATGAGTGGAGTGGTTCACCGCAGCAGNTG 1443
 1353 CGCTAACCTTTCGGGGGGAGGGCGGCCAGCGTGGATTCAGCGGCTGGGTTGAGTCTGATA 1411
 1444 AGGTAACTCTTTAGGAGCCAGCGCGCTAAGGTGGGAGAGATGATGGGTTGAGTCTGATA 1503
 1412 CAAAGTACCGGTAGG 1426
 1504 CAAAGTACCGGTAGG 1518

RESULT 14
 US-10-367-793A-3533
 ; Sequence 3533, Application US/10367793A
 ; GENERAL INFORMATION:
 ; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
 ; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome with
 ; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
 ; CURRENT APPLICATION NUMBER: US/10/367,793A
 ; CURRENT FILING DATE: 2003-02-19
 ; NUMBER OF SEQ ID NOS: 4126
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 3533
 ; LENGTH: 1102
 ; TYPE: DNA
 ; ORGANISM: Escherichia coli K-12 MG1655 complete genome with
 ; FEATURE:
 ; LOCATION: (4164692)...(4165793)
 ; OTHER INFORMATION: Chromosome - 1 Strand - positive ConnectionObjectNumber
 ; US-10-367-793A-3533

Query Match 45.8%; Score 662.6; DB 6; Length 1102;
 Best Local Similarity 78.1%; Pred. No. 6.2e-205;
 Matches 831; Conservative 0; Mismatches 210; Indels 23; Gaps 2;

412 AATGACGCTACACAGCAGAGAGCCCGCGCTAACTCGTCCAGCAGCCCGGTAAATACG 471
 24 ATTGACGCTACACAGCAGAGAGCCCGCGCTAACTCGTCCAGCAGCCCGGTAAATACG 83
 472 GAGGCGCTAGCGCTTGTTCGGAATTAATCTGGCGGTAAAGCCAGCAGTGGAGTGGAAAG 531
 84 GAGGCTGCAAGCGGTAAATCGGAATTAATCTGGCGGTAAAGCCAGCAGCGGTTTGAAG 143
 532 TCAGAGGTGAATTCACAGGCTCAACCTTGGAACTGCTTGAACCTATCATGCTGGAGT 591
 144 TCAGATGTGAATTCACCGGCTCAACCTTGGAACTGCTTGAACCTATCATGCTGGAGT 203
 592 TCAGAGAGGTGAGTGAATTCGAGGTGAGAGTGAATTCGAGTGAATTCGAGAGTGAAC 651
 204 CTCGTAGAGGGGTGAGTGAATTCGAGGTGAGAGTGAATTCGAGTGAATTCGAGAGT 263
 652 ACCAGTGGCGAGCGGCTCACTGGCTGATGCTGAGTGAATTCGAGTGAATTCGAGAGT 711
 264 ACCGTGGCGAGCGGCTCACTGGCTGATGCTGAGTGAATTCGAGTGAATTCGAGAGT 323
 712 GCAACAGAGTGAATTCACCTGCTGATGCTGAGTGAATTCGAGTGAATTCGAGAGT 771
 324 GCAACAGAGTGAATTCACCTGCTGATGCTGAGTGAATTCGAGTGAATTCGAGAGT 383
 772 AAGCATG-CTTGTGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 830
 384 GCGCTTGAAGCGGTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 443
 831 GCAAGATTAACCTCAAGGAATTCAGCGGGGCGCGCAGCAGCGGTGAGCATGTGTTT 890
 444 CCAAGGTTAACCTCAAGGAATTCAGCGGGGCGCGCAGCAGCGGTGAGCATGTGTTT 503
 891 AATTCGAGCAACCGCGAGAACCTTACCAACCTTACCAACCTTACCAACCTTACCAACCT 950
 504 AATTCGAGCAACCGCGAGAACCTTACCAACCTTACCAACCTTACCAACCTTACCAACCT 563
 951 TCAGCTTCTGCTGATGAGAGACCTGACACAGTGTGATGCTGATGCTGATGCTGATGCTG 1010
 564 GAGAATGCTGCTTTCGGGAACCGTGAAGAGTGTGATGCTGATGCTGATGCTGATGCTG 623
 1011 TGAGATGCTGCTTTCGGGAACCGTGAAGAGTGTGATGCTGATGCTGATGCTGATGCTG 1070
 624 TGAATGCTGCTTTCGGGAACCGTGAAGAGTGTGATGCTGATGCTGATGCTGATGCTG 683
 1071 AGTTGGAGTCTTATGAAACTGCGGATGATGATGATGATGATGATGATGATGATGATG 1130
 684 GCGCGGAACCTCAAGAGGAGTGCAGTGAATGATGATGATGATGATGATGATGATGATG 743
 1131 GTCTCATGCGGCTTACGGTGGGCTACACAGTGTGCTGATGCTGATGCTGATGCTGATG 1186

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Db 744 GTCATCATGCGCCCTTACGACAGGGCTACACAGTGTACATAAGGCGCATACAAGAGAA 803
QY 1187 -----GTTTAAATCCCAAAAGGACATCTCAGTTGGGATTTCTCTGTC 1228
Db 804 GCGACCTCGCGAGAGAGCGGACCTATAAAGTGGCTGTAGTCCGGATTGGAGTCTGC 863
QY 1229 AACTCGAGGCGATGAAGTTGGAATCGCTAGTAAATCGGGAAACAGCATGCCGCGTGAATA 1288
Db 864 AACTCGACTCCATGAAGTCGGATCGCTAGTAAATCGTGGATCAAGATGCCACGCGTGAATA 923
QY 1289 CGTTCGCGGCGCTGTACACACCGCGCTCACACCATGGAGTTGGTTCTTACCCGACGAC 1348
Db 924 CGTTCGCGGCGCTGTACACACCGCGCTCACACCATGGAGTTGGTTCTTACCCGACGAC 1408
QY 1349 GNTGCGCTAACTTCGCGGCGGAGGCGGCGGCGGAGTGGATTCATGATTCATGAGTGGG 1043
Db 984 GGTAGCTTAACCTTCGCGGAGGCGCTTACCACTTTGTGATTCATGAGTGGGTTGAAGTCG 1043
QY 1409 TAACAAGGTAGCGTAGGGAACCTCGCGGTGGATCACCTCCCTT 1452
Db 1044 TAACAAGGTAACTAGGGAACCTCGCGGTGGATCACCTCCCTT 1087

RESULT 15
US-10-367-793A-3357
; Sequence 3357, Application US/10367793A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome with
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,793A
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 4126
; SOFTWARE: Proprietary
; SEQ ID NO 3357
; LENGTH: 1108
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome with
; FEATURE:
; LOCATION: (4033574)...(4034681)
; OTHER INFORMATION: Chromosome - 1 Strand - positive ConnectionObjectNumber = 4477
US-10-367-793A-3357

Query Match 45.6%; Score 662.6; DB 6; Length 1108;
Best Local Similarity 78.1%; Pred. No. 6.3e-205;
Matches 831; Conservative 0; Mismatches 210; Indels 23; Gaps 2;

QY 412 ATGACGGTACGACGAGAGAGAGCCCGGCTAACTCCGTCGCCAGCAGCCGCGTAAATACG 471
Db 24 ATTGACGTTACCGCAGAGAGAGAGCCCGGCTAACTCCGTCGCCAGCAGCCGCGTAAATACG 83
QY 472 GAGGGGCTAGCGTTGCTCGGAATTACTGGCGTAAAGCGCAGCTAGGCGGACTGGAAG 531
Db 84 GAGGGTGCAGCGTTAATCGGAATTACTGGCGTAAAGCGCAGCTAGGCGGTTTGTAAAG 143
QY 532 TCAGAGGTGAATCCAGGGCTCAACTTGGAACTGCCTTGAAGATATCAGTCTGGAGT 591
Db 144 TCAGATGTGAATCCCGGGCTCAACTGGGAACTGCATCTATATCGCAAGCTTGAAT 203
QY 592 TCGAGAGAGGTGAGTGAATCCGAGTGTAGAGTGAATTCGTAGATATTCGGAGGAAC 651
Db 204 CTCGTAGAGGGGGTAGAATCCAGGTGTAGCGTGAATTCGTAGATCTGGAGGAAT 263
QY 652 ACCAGTGGCGAGGCGGCTACCTGGCTCGATGCTGAGTGGCGGAAGCGTGGGGA 711
Db 264 ACCGTGGCGAGGCGGCGGCTGGGACGAAAGACTGACGCTCAGGTGCGAAGCGTGGGGA 323
QY 712 GCAACAGGATTAGATACCTGGTGTAGTCCACCGCTTAAACGATGAATGCCACGCTCGGC 771
Db 324 GCAACAGGATTAGATACCTGGTGTAGTCCACCGCTTAAACGATGAATGCCACGCTCGGC 383
QY 772 AAGCATG-CTTGTGCGTGTACACACCTAACGGATTAAAGCATTCGCGCTGGGAGTACGGTC 830
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Db 384 GCCCTTGAGCGGTGGCTTCGCGAGCTAACGGTTAAGTCAGCCGCTGGGAGTACGGCC 443
QY 831 GCAAGATTAAGTCAAGAAATGACGGGGGCGCCACAAAGCGGTGGAGCATGTGTTT 890
Db 444 GCAAGGTTAAAGTCAAGTGAATGACGGGGGCGCCACAAAGCGGTGGAGCATGTGTTT 503
QY 891 AATTGNAAGCAAGCGCGAGAACCTTACCAACCCCTTGACATGGCAGGACCGCTGGAGAGAT 950
Db 504 AATTGATGCAAGCGGAAGAACCTTACCTGGCTTGACATCCACGGAAGTTTTCAGAGAT 563
QY 951 TCAGCTTTTCGTGAAGAGACCTGACACAGGTGCTGATGCTGCTGCTGCTGCTGCTGCTG 1010
Db 564 GAGAATGTGCTTCGCGGAACCGTGGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 623
QY 1011 TGAGATGTTGCGTTAAGTCCGGGAAACGAGCAACCCAGTCCCTAGTTCGCCACCAATTC 1070
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QY 1071 AGTTGGGAACCTTATGGAACCTGCGGATGATAGTTCGGAAGAGTGTGGATGACGTCAA 1130
Db 684 GCGCGGAACCTCAAGGAGACTGCCAGTGAATACTGGAGGAAGTGGGATGACGTCAA 743
QY 1131 GTCTCATGGGCGCTTACGGGTTGGGCTACACAGTGTCTACAATGGTGGTACACAGTGTG 1186
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QY 1187 -----GTTTAAATCCCAAAAGGACATCTCAGTTGGGATTTCTCTGTC 1228
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QY 1349 GNTGCGCTAACTTCGCGGCGGAGGCGGCGGCGGAGTGGATGATGAGTGGGTTGAAGTCG 1408
Db 984 GGTAGCTTAACCTTCGCGGAGGCGCTTACCACTTTGTGATTCATGACTGGGTTGAAGTCG 1043
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Db 1044 TAACAAGGTAACTAGGGAACCTCGCGGTGGATCACCTCCCTT 1087
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Search completed: July 28, 2003, 12:55:52
Job time : 178 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: July 28, 2003, 09:18:53 ; Search time 2887 seconds
(without alignments)
12223.796 Million cell updates/sec

Title: US-10-049-228-1
Perfect score: 1452
Sequence: 1 agttgatctctggtcgaa.....tgcggctggatcacctctt 1452

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_estl:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_est3:*
- 12: gb_est4:*
- 13: gb_est5:*
- 14: gb_est6:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description |
|------------|-------|-------|--------|----|-------------|
| 1 | 776 | 53.4 | 6499 | 28 | BH771024 |
| 2 | 686.8 | 47.3 | 899 | 29 | BZ685785 |
| 3 | 591.4 | 40.7 | 1010 | 29 | BZ431523 |
| 4 | 588.8 | 40.6 | 1053 | 29 | BZ447500 |

| | | | | | | |
|---|----|-------|------|------|----|----------|
| C | 5 | 587.2 | 40.4 | 1016 | 29 | BZ426201 |
| C | 6 | 582.8 | 40.1 | 1079 | 28 | BH705272 |
| C | 7 | 581.6 | 40.1 | 1069 | 29 | BZ474941 |
| C | 8 | 580.2 | 40.0 | 1106 | 29 | BZ469058 |
| | 9 | 566.6 | 39.0 | 1084 | 29 | BZ439740 |
| | 10 | 563.4 | 38.8 | 974 | 29 | BZ440868 |
| | 11 | 557.6 | 38.4 | 1077 | 29 | BZ450751 |
| C | 12 | 557 | 38.4 | 1054 | 28 | BH647750 |
| C | 13 | 549.8 | 37.9 | 1031 | 28 | BH656222 |
| C | 14 | 536 | 36.9 | 1044 | 29 | BZ463550 |
| C | 15 | 535 | 36.8 | 995 | 28 | BH700021 |
| C | 16 | 534 | 36.8 | 947 | 29 | BZ464837 |
| C | 17 | 531.8 | 36.6 | 1051 | 29 | BZ494182 |
| C | 18 | 530.4 | 36.5 | 1082 | 29 | BZ459110 |
| | 19 | 520.4 | 35.8 | 1020 | 28 | BH685417 |
| C | 20 | 510.4 | 35.2 | 1096 | 29 | BZ502068 |
| C | 21 | 506.4 | 34.9 | 889 | 29 | BZ426275 |
| C | 22 | 506.2 | 34.9 | 862 | 28 | BH527452 |
| C | 23 | 505.4 | 34.8 | 1143 | 28 | BH814966 |
| C | 24 | 500.2 | 34.4 | 875 | 28 | BH547523 |
| C | 25 | 499.6 | 34.4 | 857 | 28 | BH578853 |
| C | 26 | 497 | 34.2 | 848 | 28 | BH730827 |
| C | 27 | 496.8 | 34.2 | 951 | 28 | BH651765 |
| C | 28 | 496.8 | 34.2 | 955 | 29 | BZ486137 |
| C | 29 | 494.6 | 34.1 | 977 | 29 | BZ459292 |
| C | 30 | 492.8 | 33.9 | 861 | 28 | BH582045 |
| C | 31 | 491.8 | 33.9 | 623 | 14 | CD211316 |
| C | 32 | 489.4 | 33.7 | 970 | 29 | BZ494246 |
| C | 33 | 487.2 | 33.6 | 1030 | 29 | BZ463792 |
| C | 34 | 487 | 33.5 | 823 | 29 | BZ498828 |
| C | 35 | 486.8 | 33.5 | 823 | 28 | BH573967 |
| C | 36 | 485.4 | 33.4 | 865 | 28 | BH453601 |
| C | 37 | 484.8 | 33.4 | 616 | 10 | BE356988 |
| C | 38 | 481.6 | 33.2 | 845 | 28 | BH564435 |
| C | 39 | 480.8 | 33.1 | 833 | 28 | BH540327 |
| | 40 | 479.2 | 33.0 | 834 | 29 | BZ492339 |
| | 41 | 478.8 | 33.0 | 986 | 29 | BZ490055 |
| C | 42 | 478.4 | 32.9 | 935 | 29 | BZ468986 |
| C | 43 | 477 | 32.9 | 901 | 29 | BZ461852 |
| C | 44 | 475.6 | 32.8 | 861 | 29 | BZ464776 |
| C | 45 | 475.4 | 32.7 | 850 | 28 | BH677382 |

ALIGNMENTS

RESULT 1
BH771024
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BH771024
LLMGtag746 MGI363 Random Sequence Tag Library Lactococcus lactis
subsp. cremoris genomic, genomic survey sequence.
BH771024
GI:20373981
GSS.
Lactococcus lactis subsp. cremoris
Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Lactococcus.
1 (bases 1 to 6499)
Bolotin,A., Ehrlich,S.D. and Sorokin,A.
Studies of genomes of dairy bacteria Lactococcus lactis
Sci. Aliments, (2002) In press
Contact: Sorokin A
Genetique Microbienne
INRA

CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
best homologue in strain IL1403 is ywga (78%)
Class: shotgun
High quality sequence start: 30
High quality sequence stop: 6471.

| FEATURES | Location/Qualifiers |
|----------|---------------------|
| source | 1. .6499 |

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/organism="Lactococcus lactis subsp. cremoris"
/mol_type="genomic DNA"
/strain="MG1363"
/db_xref="taxon:1359"
/clone_lib="MG1363 Random Sequence Tag Library"
/note="vector: pSGM2; Site_1: Sma; Library of
chromosomal fragments of L.lactis strain MG1363 was
prepared by partial AluI digestion or by sonication."

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| BASE COUNT, * | 1946 a | 1228 c | 1683 g | 1642 t |
|---------------|--------|--------|--------|--------|
| ORIGIN | | | | |

| | | | | |
|----------------------------|--------|---------------------|------------|--------------|
| Query Match | 53.4% | Score 776; | DB 28; | Length 6499; |
| Best Local Similarity | 73.7%; | Pred. No. 1.5e-202; | | |
| Matches ll34; Conservative | 0; | Mismatches 316; | Indels 89; | Gaps 8; |

| | | | |
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| QY | 1 | AGTTTGATCCTGCTGCAGAACGAAACGCTGCGCGCAGGCTTTAAACACATGCAAGTCGAGCGA | 60 |
| Db | 534 | AGTTTGATCCTGCTGCAGAACGAAACGCTGCGCGCAGGCTTTAAACACATGCAAGTCGAGCGA | 593 |
| QY | 61 | G-----ACCTTCGGGTCTAGCGCGGACGCGGTGAGTAAACGCT-GGGAA | 103 |
| Db | 594 | TGAAGATTGGTTCACCAATTTGAAGAGCAGCAACGGGTGAGTAAACGCTGGGGAA | 653 |
| QY | 104 | CGTGCCTTCTCTACGGAATAGCCCGGGAAACTTGGGAGTAAATACCGTATACGCCCTTTG | 163 |
| Db | 654 | TCTCGCTTTGAGCGGGGACAACATTTGGAACGAATGCTAAATACCGCATAAACTTTA | 713 |
| QY | 164 | GGGGAAGAATT-----ATCGGAGAAGATCGGCCCGCTTGGGA | 202 |
| Db | 714 | AACATAAGTTTAAAGTTTGAAGATGCAATTTGATCACTCAAAGATGATCCCGCTTGTA | 773 |
| QY | 203 | TTAGGTAGTTGGTGGGTAAATGCCCAACCAACCGGACGATCCATAGCTGTTTTCAGAGGA | 262 |
| Db | 774 | TTAGCTAGTTGGTGAAGTAAAGGCTCACCAGGCGGATGATACATAGCCGACCTTGAGAGGG | 833 |
| QY | 263 | TGATCAGCCACACTGGGACTTGAGACACGCGCCAGACTCCTACGGAGGACAGCAGTGGGA | 322 |
| Db | 834 | TGATCGGCCACATTTGGGACTTGAGACACGCGCCAACTCCTACGGAGGACAGCAGTAGGA | 893 |
| QY | 323 | ATCTTAGACAAATGGGGCACCTGATCTAGCCATGCCGCGTGAGTGATGAAGGCCCTTAG | 382 |
| Db | 894 | ATCTTCGGCAATGGACGAAGTCTGACCGAGCAACCGCGGTGAGTGAAGAGGTTTTTCG | 953 |
| QY | 383 | GTTTGTAAAGCTCTTTTCAGCTGGGAAGAT-----AATGA | 416 |
| Db | 954 | GATCGTAAAACTCTGTTGGTGAAGAGAAGCTGTTGGTGAGAGTGGAAGCTCATCAAGTGA | 1013 |
| QY | 417 | CGGTACCGACGAGAAGACCCCGGCTAACTCCGTGCCAGCAGCCGGGTAAATACGAGGG | 476 |
| Db | 1014 | CGGTAACTACCCAGAAGGACGCGCTAACTACGTGCCAGCAGCGCGGTAAATACGTAGT | 1073 |
| QY | 477 | GGCTACGCTGTTTCGGAAATTACTTGGCGTAAAGCGCACGTPAGCGGACTTGAAGTCAGA | 536 |
| Db | 1074 | CCCGACGTTGCCGGATTATTGGCGGTAAACGAGCGCAGGTGTTATTAAAGTCTGG | 1133 |
| QY | 537 | GGTGAATCCGAGGCTCAACCTTGGAACTGCCCTTTGAAACTATCAGTCTGGAGTTCGAG | 596 |
| Db | 1134 | TGTAAAAGGCGATGGCTCAACCAATTGTA-TGCATTGGAAACTGGTAGACTTGAGTSCAGG | 1192 |
| QY | 597 | AGAGGTGAGTGGAAATCCGAGTGTAGAGGTGAATTTGTTAGATATTTCGGAGGGAACACCAG | 656 |
| Db | 1193 | AGAGGAGATGGGAATTTCCATGTGTACGGGTGAATTCGTAGATATATGGAGGGAACACCGG | 1252 |
| QY | 657 | TGCGAAGCGCGCTCACTGGCTCGATACCTGACGCTGAGGTGCCAAAGCGGTGGGGAGCAAA | 716 |
| Db | 1253 | TGSCGAAAGCGGCTCTGSCCTGTAACTGACACTGAGGCTCGAAGCGCTGGGGAGCAAA | 1312 |
| QY | 717 | CAGGATTAGATCCCTGGTAGTCCACCGCGTAAACGATGAATGCCAGACGCTCGGCAAGCA | 776 |
| Db | 1313 | CAGGATTAGATACCTTGGTAGTCCACCGCGTAAACGATGAGTCTAGATCTAGATCTAGGAGCTA | 1372 |

| | | | | | | | | |
|----|------|------------------|------------------|------------------|-------------------|-------------|----------|------|
| Qy | 777 | T-GCTTCTCGGTGTCA | CACCACTTAACGGATT | TAAGCATTC | CGCTCGGGAGTACGGT | CGCAAG | 835 | |
| | | | | | | | | |
| | | | | | | | | |
| Db | 1373 | TAAGTTCTCTGTATC | GCAGCTTAACGCAAT | TAAGCACTCCGCT | GGGAGTACGACCGCAAG | 1432 | | |
| | | | | | | | | |
| Qy | 836 | ATTAATAACTCAAA | GAGGAATTGACGGG | GCCCGCACAAAGCGGT | GGAGCATGTGGTTT | AATTTC | 895 | |
| | | | | | | | | |
| Db | 1433 | GTTGAACACTCAAA | GAGGAATTGACGGG | GCCCGCACAAAGCGGT | GGAGCATGTGGTTT | AATTTC | 1492 | |
| | | | | | | | | |
| Qy | 896 | GAGCAACGCGCAGA | CACTTTACCAACCTT | TGACATGGCAGG | ACCGCTGGAGATTC | CAGC | 955 | |
| | | | | | | | | |
| Db | 1493 | GAAGCAACGGAGAA | CACTTACCAAGTCTT | TGACATCTCGTGT | ATTCTTAGAGATAGGA | 1552 | | |
| | | | | | | | | |
| Qy | 956 | TTTCTCTAAGAGAC | CTGCACACAGGTG | CTGCATGGCTGTC | GACGCTCGTCTG | GTGAGA | 1015 | |
| | | | | | | | | |
| Db | 1553 | AGTTCCTTCGGGAC | ACGGGATACAGTGGT | GCATGGTTGTC | GTCAGCTCGTCTG | GTGAGA | 1612 | |
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| Qy | 1016 | TGTTTCGGTTAAGT | CCGGCAACAGCGC | CAACCCACGTC | CCCTAGTTGCCAGCA | ATTCA | 1075 | |
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| Db | 1613 | TGTTGGGTTAAGT | CCCGCAACAGCGC | CAACCCCTATT | TGTTAGTTGCCATC | -ATTAAGTTG | 1671 | |
| | | | | | | | | |
| Qy | 1076 | GGAACCTCTATG | GGAACCTGCCGAT | GATAAAGTC | GAGGGAAGGTGT | GGATGACGTC | CAAGTCCT | 1135 |
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| Db | 1672 | GGCACTCTAAC | GAGACATGCGCGGT | GATAAACCGGAGGA | AGGTGGGGATGAC | GTCAAAATCAT | 1731 | |
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| Qy | 1136 | CATGGGCTTTAC | GGGTTGGGCTAC | ACAGCTGCTAC | AAATGCTGTGTG | ACAC | ----- | 1183 |
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| Db | 1732 | CATGCCCTTTAT | GAACCTGGGCTAC | ACAGTGCAT | AGTGCATAGGAT | GGTACACGAGT | CGGGAG | 1791 |
| | | | | | | | | |
| Qy | 1184 | -----GTGGGTT | TAATCCCAAAAGGC | ATCTCAGTT | CGGATTTGCTCT | GTGCAACTC | 1233 | |
| | | | | | | | | |
| Db | 1792 | ACAGTGATGTT | AGCTAATCTCT | TAAACCACTTCT | CAGTTCCGAT | TGTAGGCTGCA | ACTC | 1851 |
| | | | | | | | | |
| Qy | 1234 | GAGGGCATGA | GTTGGAAATCGCT | AGTAAATCGCGG | ACACAGCATCGCGGGT | TGAATAC | GTTC | 1293 |
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| Db | 1852 | GCCTACATGA | GTCGGAAATCGCT | AGTAAATCGCGG | ATCAGCACGCGCGGT | TGAATAC | GTTC | 1911 |
| | | | | | | | | |
| Qy | 1294 | CCGGGCTTGT | ACACACCGCGCT | CAACCATGGG | AGTTGTTCTAC | CCGACACG | CTGC | 1353 |
| | | | | | | | | |
| Db | 1912 | CCGGGCTTGT | ACACACCGCGCT | CAACCATGGG | AGTTGTTGAG | TACCCGAA | TAGGTTG | 1971 |
| | | | | | | | | |
| Qy | 1354 | GCTAAACCTTC | GGGGGACGCGG | CCAGTGGAT | CAGCGACTGGG | GTGAAGT | TCGTAACA | 1413 |
| | | | | | | | | |
| Db | 1972 | CCTAAACCGA | AGGAGGCGCTT | CCTAAGGTAA | AGACCGATGACT | GTGGGTGA | GTGTAACA | 2031 |
| | | | | | | | | |
| Qy | 1414 | AGGTAGCCGT | AGGGGAACCT | TCGGCTGGAT | CACTCCTCTT | 1452 | | |
| | | | | | | | | |
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| | | | | | | | | |

RESULT 2
BZ685785/c
LOCUS
DEFINITION BZ685785 899 bp DNA linear GSS 05-FEB-2003
PUBD754TD ZM.0_6_1.0.KB Zea mays genomic clone ZMMBTA032112,
genomic survey sequence.
ACCESSION BZ685785
VERSION BZ685785.1 GI:28245311
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 899)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick
A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennetzen,J.
Maize Genomics Consortium
Unpublished
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org

Db 710 TGGGGTAAAGCGTCTGTAGTGGCTTTTAAAGTCCGGCTCAATCCAGGGCTCAACC 651
QY 559 TTGGAAGTCCTTTGAACTATCATCTGAGTTCGAGAGAGGTGAGTGAATCCCGAGT 618
Db 650 CTGGACAGCGGTGAAACTACCAAGCTTGAGTACGGTAGGGCAGAGGGAATTCGCGT 591
QY 619 CTAGAGGTGAATTCGTAGATATTCGGAGGACACCACTGCGGAGGCGGTCTACTGGCT 678
Db 590 GGAGCGGTGAATTCGTAGATATTCGGAAGAACCAACCAAGCAAGCACTCTGCTGGGC 531
QY 649 CGATACCTGACCTGAGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 738
Db 530 CGACACTGACACTGAGAGACCAAGCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 471
QY 739 CCACGCCGTAAACGATGAATCCAGAGC--TCGCAAGCATCTGTGTCGTCGTCACACCT 796
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QY 797 AACGGATTAACGATTAACGATTAACGATTAACGATTAACGATTAACGATTAACGATTA 856
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QY 857 CGGGGGCCGACAAAGCGGTGAGCATGTGTTTAAATTCGAAGCAACGCGAGAACCTTA 916
Db 350 CGGGGGCCGACAAAGCGGTGAGCATGTGTTTAAATTCGAAGCAACGCGAGAACCTTA 291
QY 917 CCAACCTTGATCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 976
Db 290 CCAAGGCTTGATCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 231
QY 977 ACAGGTGTCGATCGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1036
Db 230 ACAGGTGTCGATCGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 171
QY 1037 GAGCGCAACCAAGCGTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1096
Db 170 GAGCGCAACCAAGCGTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 112
QY 1097 ATGATAAGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1156
Db 111 GTGATAAGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 52
QY 1157 TACACAGTGTACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1189
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DEFINITION BONKF40TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONKF40,
genomic survey sequence.
ACCESSION BZ447500
VERSION BZ447500.1 GI:26712943
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 1053)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished
Other GSSs: BONKF40TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdownt@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR

Class: sheared ends.
Location/Qualifiers
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total DNA inserted into pHD1 using BstXI linkers"
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Best Local Similarity 76.8%; Pred. No. 12.8e-151;
Matches 771; Conservative 0; Mismatches 227; Indels 6; Gaps 4;
QY 190 GGGCGCGCTGGATTAGTGTGGGTAAATGCCCAAGCGAGTCCATAGC 249
Db 1052 GGGTCCGCTCTGATTAGTGTGGGTAAATGCCCAAGCGAGTCCATAGC 993
QY 250 TGGTTGAGAGGATCATCAGCCACACTGGGACTGAGACACGCCCGAGTCCCTACGGGAG 309
Db 992 TGGTCCGAGAGGATCATCAGCCACACTGGGACTGAGACACGCCCGAGTCCCTACGGGAG 933
QY 310 GCAGCAGTGGGGAATCTTAGACAATGGGGCAACCTGATCTAGCCATGCCGCTGAGTG 369
Db 932 GCAGCAGTGGGGAAT-TCGCCGAATGGGGCAAGCTGACGGAGCAATGCCGCTGAGG 874
QY 370 ATGAGGCGCTTAGGGTTGTTAAAGCTCTTTTACGCTGGGAAGA--TAATGACGTTACAGCA 427
Db 873 TAGAAGGCGCTACGGGCTCTGAACTTTTCCAGAGAAGAAGCAATGACGCTATCTGGG 814
QY 428 GAAGNAAGCCCGGCTAACTCCGTCGACAGCAGCGGGTAAATACGGAGGGGCTACGTTG 487
Db 813 GAATAAGCATCGGCTAACTCTGTGCGCAGCAGCGGGTAAATACAGAGGATGCAAGCGTTA 754
QY 488 TTCGGAATTAATCTGGCGTAAAGCGCACCTAGCGGACTGGAAGTACAGAGTGAATCC 547
Db 753 TCCGGAATTAATCTGGCGTAAAGCGTCTGTAGTGGCTTTTAAAGTCCCGCTCAATCC 694
QY 548 AGGGCTCAACCTTGGAACTGCTTGAACATATCATCTGAGTTCGAGAGAGGAGTGAGTG 607
Db 693 AGGGCTCAACCTTGGAACTGCTTGAACATATCATCTGAGTTCGAGAGAGGAGTGAGTG 634
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Db 573 CTCTGCTGGCGGACACTGACACTGAGAGACGAAAGCTAGGGAGGCGAATGAGTATAGAT 514
QY 728 ACCCTGTTAGTCCAGCGCTAAACATGAATGCCAGAGC--TCGCGAAGCATGCTGTGCG 785
Db 513 ACCCGAGTGTCTAGCGTAAACATGATGATAGTCTGAGGCTGTGCTGATCGACCGGTGCA 454
QY 786 GTGTACACCTTAACGATTAACGATTAACGATTAACGATTAACGATTAACGATTAACGAT 845
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QY 846 AAAGGAATTAACGATTAACGATTAACGATTAACGATTAACGATTAACGATTAACGATTA 905
Db 393 AAAGGAATTAACGATTAACGATTAACGATTAACGATTAACGATTAACGATTAACGATTA 334
QY 906 GCAGAACCTTAACGATTAACGATTAACGATTAACGATTAACGATTAACGATTAACGAT 965
Db 333 GAAGAACCTTAACGATTAACGATTAACGATTAACGATTAACGATTAACGATTAACGATTA 274
QY 966 GAGACCTCAACGATTAACGATTAACGATTAACGATTAACGATTAACGATTAACGATTA 1025
Db 273 GGAACGCGGACAGGATTAACGATTAACGATTAACGATTAACGATTAACGATTAACGATTA 214

QY 1026 AGTCCGCGACGAGCGCAACCCAGCTCCCTAGTTGCGCAGCAATTCAGTTGGAACTCTAT 1085
 DB 213 AGTCCGCGACGAGCGCAACCCCTGTTTATAGTTGCCA-CGGTTGAGTTGGAACTCTGA 155
 QY 1086 GGAATCTCCGATGATTAAGTCGCGAGGAGGTGGATGAGTCAAGTCCCTCATGGGCTT 1145
 DB 154 ACAGACTGCGCGGTGATAAGCGGAGGAGGTGAGTCAAGTCAATCATGATCCGCTT 95
 QY 1146 ACGGTTGGCTACACAGCTGCTACAAATGTTGGTGACAGTGGGT 1189
 DB 94 ATGCCCTGGCGGACACACAGTGTACAAATGCGCGGACAAAGGT 51

RESULT 5
 B2426201/c
 LOCUS B2426201 1016 bp DNA linear GSS 13-DEC-2002
 DEFINITION BOND228TF BO.1.6_2_KB_tot Brassica oleracea genomic clone BOND228,
 genomic survey sequence.
 ACCESSION B2426201
 VERSION B2426201.1 GI:26667713
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 1016)
 Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
 TITLE Whole genome shotgun sequencing of Brassica oleracea
 JOURNAL Unpublished
 COMMENT Other_GSSs: BOND228TR
 Contact: Chris Town

TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.

FEATURES
 source
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 /mol_type="genomic DNA"
 /strain="Tol000DH3"
 /db_xref="taxon:3712"
 /clone="BOND228"
 /note="Vector: PHOS1; Site 1: BstXI; 1.6-2 kb sheared
 total DNA inserted into PHOS1 using BstXI linkers"

BASE COUNT 193 a 328 c 239 g 256 t
 ORIGIN

Query Match 40.4%; Score 587.2; DB 29; Length 1016;
 Best Local Similarity 76.7%; Pred. No. 7.7e-151;
 Matches 770; Conservative 0; Mismatches 228; Indels 6; Gaps 4;

QY 190 GCGCCGCTGGATAGTATAGTTGGTGGTAAATGCCCCACCAAGCGGATCCATAGC 249
 DB 1015 GCGTCGGCTGATAGTATAGTTGGTGGTAAATGCCCCACCAAGCGGATCCATAGC 956
 QY 250 TGGTTTCAGAGGATGATCAGCCACATGGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 309
 DB 955 TGGTCCAGAGGATGATCAGCCACATGGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 896
 QY 310 GCAGCAGTGGGATCTTAGCAATGAGCAACCTGATCTAGCCATGCGCGTGAGTG 369
 DB 895 GCAGCAGTGGGATCTTAGCAATGAGCAACCTGATCTAGCCATGCGCGTGAGTG 837
 QY 370 ATGAAGCCCTTAGGTTGTAAGCTCTTTTCAGCTGGGAAGA--TAATGACGGTACCAGCA 427
 DB 836 TAGAAGCCCTTAGGTTGTAAGCTCTTTTCAGCTGGGAAGA--TAATGACGGTACCAGCA 777

QY 428 GAAGAAGCCCGGCTAACTCCGTGCGCAGCAGCCGCGTAAATACGAGGGGGCTAGCGTTG 487
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 QY 488 TTCGGAATTAATCGGCGTAAAGCGACGTAGCGGACCTGGAAAGTCAGAGGTGAAATCCC 547
 DB 716 TCCGGAATTAATCGGCGTAAAGCGCTCTGTAGTGGCTTTTAAAGTCCCGCTCAATCCC 657
 QY 548 AGGCTCAACCTTGGAACTGCTTGAACATATCATCTGGAGTTCGAGAGAGGTGAGTG 607
 DB 556 AGGCTCAACCTTGGAACTGCTTGAACATATCATCTGGAGTTCGAGAGAGGTGAGTG 597
 QY 608 GAATTCGAGTGTAGAGGTGAAATTCGTAGATATATTCGGAGAACACACCTAGTGGCGG 667
 DB 596 GAATTCGAGTGTAGAGGTGAAATTCGTAGATATATTCGGAGAACACACCTAGTGGCGG 537
 QY 668 GCTCAGTGGCTGATGATGAGTGTAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 727
 DB 536 CTCTGCTGGCGGACACTGACACTGAGAGACGAAAGCTAGGGAGCGAATGGGATAGAT 477
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 QY 966 GAGACCTGCACACAGGTGCTGATGGCTGTGCTGAGTGTGCTGCTGAGATGATCGGTTA 1025
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 QY 1146 ACGGTTGGCTACACAGCTGCTACAAATGTTGGTGACAGTGGGT 1189
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 DEFINITION BOMKA47TF BO.2_3_KB Brassica oleracea genomic clone BOMKA47,
 genomic survey sequence.
 ACCESSION BH705272
 VERSION BH705272.1 GI:18787746
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 1079)
 Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
 TITLE Whole genome shotgun sequencing of Brassica oleracea
 JOURNAL Unpublished
 COMMENT Other_GSSs: BOMKA47TR
 Contact: Chris Town

QY 120 GAATAGCCCGGGAACCTGGAGTAATACCGTATACGCCCTTTGGGGAAAGATTAT-C 178
 Db 936 GAACACACAGCTGGAAACGGCTGCTAATACCCGTAGGCTGAGGACAAAGAGGAATCC 877
 QY 179 GGAGAAGGATCGCGCGGCTGGATTAGTGTAGTGGTGGTAAATGGCCCAACGACCGA 238
 Db 876 GCCGAGGAGGGCTCGGCTGATTAGTGTAGTGGTGGTAAATGGCCCAACGACCGA 817
 QY 239 CGATCCATAGCTGTTGAGAGGATGATACGCCACATGGGACATGAGACGCGCCAGAC 298
 Db 846 TGATCAGTAGCTGTCGAGAGGATGATACGCCACATGGGACATGAGACGCGCCAGAC 757
 QY 299 TCCTACGGAGGACGAGTGGGATCTTACACATGGGACACCCCTGATCTAGCCATG 358
 Db 756 TCCTACGGAGGACGAGTGGGATCTTACACATGGGACACCCCTGATCTAGCCATG 697
 QY 359 CCGGTGATGATGAAGCCCTTAGGTTGTAAAGCTCTTTCAGCTGGGAAGA--TAATGA 416
 Db 696 CCGGTGATGATGAAGCCCTTAGGTTGTAAAGCTCTTTCAGCTGGGAAGA--TAATGA 637
 QY 417 CGGTACACAGCAGAACGCCCGGCTAACTCCGTGCCAGCAGCCCGGTAAATACGAGGG 476
 Db 636 CGGTATCTGGGAATACCATCGCTAACTCTGTGCCAGCAGCCCGGTAAATACGAGGA 577
 QY 477 GGCTAGCGTTCTTCGGAATTAATCTGGGCTAAAGCGCTAGGCGGACTGGGAAGTCAGA 536
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 QY 775 CATGCTTCTGCTGATCAGCTAACGGATTAAGCATTCGCTGGGAGTACGCTGCGAA 834
 Db 276 CGACCGGTGATGCTGTGATTAACCGCTTAAGTATCCGCTGGGAGTACGCTGCGAA 217
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 Db 216 GAATGAAGCACTCAAGGAATGACGGGGCCGCAACAGCGGTGGAGCATGTGTTTAATT 157
 QY 895 CGAGCAACGCGAGCACTTACCAACCTTGACATGGAGGACCGCTGGAGAGATTGAG 954
 Db 156 CGATGCAAGGGAAGCACTTACCAAGCGCTTACATGCGCGCAATCTCTTGAAGAGAG 97
 QY 955 CTTTCTCTGATGAGACCTGACACAGGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 1014
 Db 96 GGGTCCCTTCGGGAACGCGGACAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 37
 QY 1015 ATGTTTGGTTAAGTCCGCAACGAGCGCAACCCAG 1050
 Db 36 GTATTGGTTAAGTCCGCAACGAGCGCAACCCCTCG 1

RESULT 8

B2469058/c

LOCUS

DEFINITION

BONHE54TF BO.1.6.2_KB_tot Brassica oleracea genomic clone BONHE54,

genomic survey sequence.

ACCESSION

B2469058

VERSION

B2469058.1

GI:26764665

KEYWORDS

GSS

SOURCE
 ORGANISM
 Brassica oleracea
 Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE
 1 (bases 1 to 1106)
 AUTHORS
 Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
 TITLE
 Whole genome shotgun sequencing of Brassica oleracea
 JOURNAL
 Unpublished
 COMMENT
 Other_GSSs: BONHE54TR
 Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: shared ends.
 Location/Qualifiers
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 /note="Vector: PHOS1. Site 1: BatXI; 1.6-2 kb sheared
 total DNA inserted into PHOS1 using BstXI linkers"
 BASE COUNT 211 a 360 c 255 g 280 t
 ORIGIN

Query Match 40.0%; Score 580.2; DB 29; Length 1106;
 Best Local Similarity 74.9%; Pred. No. 6.8e-149;
 Matches 792; Conservative 0; Mismatches 258; Indels 7; Gaps 5;
 QY 1 AGTTTGTATCTGGCTCAGAACGACGCTGGCGCAGCTTAACACATGCAAGTCGACGCA 60
 Db 1077 AGTTTGTATCTGGCTCAGAACGACGCTGGCGCAGCTTAACACATGCAAGTCGACGCA 1018
 QY 61 GACCT-TCGGGTCTAGCGCGGACGCGGTGAGTAACCGTGGGACGCTGCCCTTCTCTACG 119
 Db 1017 GAAGTGGTGTTCAGAGTGGCGGCGGTGAGTAACCGTGGGACGCTGCCCTTCTCTACG 959
 QY 120 GAATAGCCCGGAAACTGGGAGTAATACCGTATACCGCTTTGGGGGAAAGATTAT-C 178
 Db 958 GACACCCAGCTGGAAACGCGCTGCTAATACCCGTAGCTGAGGAGCAAGAGGATATCC 899
 QY 179 GGAGAAGGATCGCCCGCGCTGGATTAGTGTAGTGGGTAAATGCCCAACGACCGCA 238
 Db 898 GCCCGAGGAGGGGCTCGCGCTCTGATTAGTGTAGTGGTAAATAGCTTACCAAGCGCA 839
 QY 239 CGATCCATAGCTGGTTTGAGAGGATGATCAGCCACACTGGGACTGAGACACGCCCCAGAC 298
 Db 838 TGATCAGTAGCTGGTCCGAGAGGATGATCAGCCACACTGGGACTGAGACACGCCCCAGAC 779
 QY 299 TCCTACGGGAGGACGAGTGGGAATCTTAGACAATGGGGCAACCTTGATCTAGGCATG 358
 Db 778 TCCTACGGGAGGACGAGTGGGAATCTTAGACAATGGGGCAACCTTGATCTAGGCATG 719
 QY 359 CGCGCTGATGATGAGGCGCTTAGGGTTGTAAGCTCTTTTACAGCTGGGAAGA--TAATGA 416
 Db 718 CGCGCTGAGGTAGAGGCGCTACGGGTCTCTGAACTCTTTTCCAGAGAGAGGATGA 659
 QY 417 CGGTACACAGCAAGAACGCCCGGCTAACTCCGTGACGAGCGCGGTAAATACGAGGG 476
 Db 658 CGGTATCTGGGAATTAAGCATCGCTAACTCTGTGCGACGAGCGCGGTAAATACGAGGA 599
 QY 477 GGTAGCTGTGTTCGGAATTAAGTGGGCTAAAGCGACGCTGAGGAGTGGGAGTGGAG 536
 Db 598 TGAACGCGTTATCCCGGAATGATGGGCGTAAAGCGTCTGAGTGGCTTTTAAAGTCCG 539
 QY 537 GGTGAATCCAGGCTCAACTTGGAACTGCTTTGAACTATCATGCTGGAGTTCGAG 596

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Db 538 CGTCAATCCAGGGCTCAACCGTGGACAGCGGTGAAACTACCAAGCTTGAGTACGGT 479
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Db 478 AGGGGAGAGGGAATTCGCGTGGAGCGGTGAATTCGAGATATTCGGAGGAAACACCAA 419
QY 657 TGGCGAAGCGGGCTCACTGGCTGATACCTGACCTGAGGTGCGAAAGCGTGGGAGCAAA 716
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QY 775 CATGCTTGTGCGGTGTCACACCTAACGATTAACGATTCGCGCTGGGGAGTACGGTCGCAA 834
Db 298 CGACCGGTGAGTGTGTAGTAAACGCTTAAGTATCCCGCTGGGGAGTACGTTGCGAA 239
QY 835 GATTAACCTCAAGGAATTCAGCGGGCGGCGCACAGCGGTGGAGCATGTGTTAAAT 894
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Db 118 GGTGCTTGGGAACCGGACACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 59
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LOCUS BZ439740 1084 bp DNA linear GSS 13-DEC-2002
DEFINITION BONDUS4TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONDUS4,
genomic survey sequence.
ACCESSION BZ439740
VERSION BZ439740.1 GI:26695676
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 1084)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished
Other_GSSs: BONDUS4TR
Contact: Chris Town
```

```
TIGR
712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
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Location/Qualifiers
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/clone="BONDUS4"
/notes="Vector: pHS1; Site 1: BstXI; 1.6-2 kb sheared
total DNA inserted into pHS1 using BstXI linkers"
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Best Local Similarity 74.4%; Pred. No. 3.8e-145;
Matches 791; Conservative 0; Mismatches 244; Indels 28; Gaps 5;
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QY 291 GCCAGACTCTCTAGCGGAGCGAGCAGTGGGGAATCTTAGACAATGGGGGCAACCCCTGATC 350
Db 66 GCCAGACTCTCTAGCGGAGCGAGCAGTGGGGAATTTCCCGCAATGGGGGAAAGCCTGAGC 125
QY 351 TAGCCATCGCGGTGAGTGTAGAGGCTTAGGGTGTAAAGCTCTTTCAGCTGGGAAGA 410
Db 126 GAGCAATGCCGCGTGGAGGTAGAAAGGCTAGGGTCTCTGAACTCTTTTCCAGAGAGA 185
QY 411 --TAATGACGTACACAGCAAGAACGCCGCTAACTCCGTCGACGAGCGCGGTAAAT 468
Db 186 AGCAATGACGTATCTGGGGAATPAGCATCGCTACTCTGTGCGAGCGCGCGGTAAAT 245
QY 469 ACAGAGGGGCTAGCTGTGTTGGAATPACTTGGCGGTAAAGCGCACGCTAGGCGGACTGGA 528
Db 246 ACAGAGGATGCAAGCGTTATCCCGAATGATGGCGGTAAAGCGTCTGTAGGTGGCTTTT 305
QY 529 AAGTCAGAGTGAATCCAGGGCTCAACCTTGAACCTGCTTTGAAACTATCAGTCTGG 588
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QY 589 AGTTCGAGAGGTGAGTGAATTCGAGTGTAGAGGTGAATTCGTAGATATTCGAGG 648
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Db 426 AACACCAACGCGGAAGCACTCTCTGCGGCGACACTGACACTGAGAGACGAAAGCTAGG 485
QY 709 GGAGCAAAAGGATTAATACCTGAGTGTAGTCCAGCGCTAAACGATGAATGCCAGACGTC 768
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QY 887 GTTTAATTCGAAGCAACGCGCAGAACCTTACCAACCTTACATGCGGAGGACCGGTGAG 946
Db 666 GTTTAATTCGATGCAAGCGAAGAACCTTACAGGGGCTTGACATGCCCGCAATCTCTTG 725
QY 947 AGATTGAGCTTCTCGTAAAGACCTGCACACAGTGTGCTGATGCTGCTGCTGCTGCTGCT 1006
Db 726 AAAGAGAGGGGTGCTTCGGGAACGCGGACACAGGTGCTGCTGCTGCTGCTGCTGCTGCT 785
QY 1007 GTGCTGAGATGTTTCGGTTAAAGTCCGCAACGAGCGCAACCCACCTGCTTCTGCTGCA 1066
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QY 1067 ATTGAGTTGGAACTCTATGGAACCTCCGATGATAAGTCGAGAGAGGTTGATGATGACG 1126
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| QY | 1229 | AACTCAGGCGCATGAAGTTGGAAATCGCTAGTAAATCGCGGAACAG-CATCGCGGGTGAAT | 1287 |
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| Db | 907 | AACTCGCCTGCATGAAGCGGAATCCGCTAGTATCCCGGTAGCCCATACGGCGGTGAAT | 966 |
| QY | 1288 | ACGTTCCCGGGGCTTGTACACACCCGCCGCTACACACCATGGAGTTGGTTCTATCCCGACGA | 1347 |
| Db | 967 | TGTTCCCGGGGCTTGTACACACCCGCCGCTACACACTATGGAGCTATGGCCATGCCGGAAG | 1026 |
| QY | 1348 | CGNTGGCTTAACCTTCGGGGGCGACGGCCACCGGTAGGATCAGCCACTGG | 1398 |
| Db | 1027 | TGCTACTCTTAACCCGAGGAGGGGGTGCAGAGGCGGGCTAGTACTGG | 1077 |
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| BH647750/c | | | |
| LOCUS | BH647750 | 1054 bp | DNA linear |
| DEFINITION | BOMND31TR BO_2_3_KB Brassica oleracea genomic clone BOMND31, | | GSS 19-FEB-2002 |
| ACCESSION | BH647750 | | genomic survey sequence. |
| VERSION | BH647750.1 | GI:18705298 | |
| KEYWORDS | GSS. | | |
| SOURCE | Brassica oleracea | | |
| ORGANISM | Brassica oleracea | | |
| REFERENCE | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | |
| AUTHORS | Spezmatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids | | |
| TITLE | ; eurosids II; Brassicales; Brassicaceae; Brassica. | | |
| JOURNAL | 1 (bases 1 to 1054) | | |
| COMMENT | Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished Contact: Chris Town | | |
| FEATURES | | | |
| source | TIGR | | |
| | 9712 Medical Center Drive, Rockville, MD 20850, USA. | | |
| | Tel: 301-838-3523 | | |
| | Fax: 301-838-0208 | | |
| | Email: cdtown@tigr.org | | |
| | Seq from: a doubled haploid provided by Tom Osborn. | | |
| | Seq primer: TR | | |
| | Class: sheared ends. | | |
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| | /note="Vector: pHOs1; Site:1. BstXI; 2-3 Kb sheared | | |
| | genomic DNA inserted into pHOs1 using BstXI linkers" | | |
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| ORIGIN | | | |
| | Query Match 38.4%; Score 557; DB 28; Length 1054; | | |
| | Best Local Similarity 74.4%; Pred. No. 1.7e-142; | | |
| | Matches 778; Conservative 0; Mismatches 241; Indels 27; Gaps 5; | | |
| QY | 432 | ANGCCCCGGCTAACTCCGTTGCCAGACGCCGGGTAAATACGGAGGGGCTAGCGTTGTCG | 491 |
| Db | 1054 | AAGCATCGCTAACTCTGTGCCAGACGCCGGTAAATACAGAGGATGAAGCGTTATCCG | 995 |
| QY | 492 | GAATTACTTGGCGTAAAGCGCAGTATGGCGGACTGGAAGTCAGAGGTGAATATCCAGGG | 551 |
| Db | 994 | GAATGATTTGGCGTAAAGCGTCTGTAGTGG-CTTTTAAAGTCCCGCGTCAATATCCAGGG | 936 |
| QY | 552 | CTCAACCTTGAACCTGCCTTTGAAACTATCAGTCTGGAGTTCCGAGAGAGGTGAGTGAAT | 611 |
| Db | 935 | CTCAACCTTGGACAGCGGTGGAACCTACCAAGCTTGAGTACGGTAGGGCAGAGGAAT | 876 |
| QY | 612 | TCCGAGTGTAGAGTGAATTCGTAGATATTCGGAGGACACACCACTGGCGAGGCGGCTC | 671 |
| Db | 875 | TTCCGGTGGCGGTGAAATCGGTAGAGATCGGAAAGACCAACCGCGGAAGACACTCT | 816 |

[illegible]

LOCUS BH700021 995 bp DNA linear GSS 20-FEB-2002
 DEFINITION BOMND50TR BO_2_3_KB Brassica oleracea genomic clone BOMND50,
 genomic survey sequence.
 ACCESSION BH700021
 VERSION BH700021.1 GI:18775982
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 * : eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 995)
 TOWN, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished
 Other GSSs: BOMND50TF
 Contact: Chris Town

TIGR Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208

Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR
 Class: sheared ends.

FEATURES

Location/Qualifiers
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 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="TO1000DH3"
 /db_xref="taxon:3712"
 /clone="BOMND50"
 /clone_lib="BO_2_3_KB"
 /note="Vector: pHOS1. Site 1: BstXI. 2-3 kb sheared
 genomic DNA inserted into pHOS1 using BstXI linkers"

BASE COUNT
 181 a 330 c 226 g 258 t

Query Match 36.8%; Score 535; DB 28; Length 995;
 Best Local Similarity 73.8%; Pred. No. 1.9e-136;
 Matches 734; Conservative 0; Mismatches 255; Indels 6; Gaps 4;

| | | | |
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| QY | 16 | CAGAACGACGCTGGCGCAGGCTTAACACATGCAAGTCGACGAGACCT-TCGGGTCTTA | 74 |
| Db | 995 | CAGGATGACGCTGGCGGCATGCTTAACACATGCAAGTCGACGGAAGTGGTGTTC | 936 |
| QY | 75 | CGCGCGGACGGGTAGTAAACGGTGGGAACGTCCTCTCTACGGAATAGCCCGGAA | 134 |
| Db | 935 | GTGGCGGACGGGTAGTAAACGGTGGGAACGTCCTCTCTACGGAATAGCCCGGAA | 876 |
| QY | 135 | ACTGGGAGTAATACCGTATACCCCTTTGGGGGAAGATTAT-CGAGAAGATCGGCC | 193 |
| Db | 875 | ACGGTGTCTAATACCCGTAGCTGAGNGCAAGAGGAATCCCGCAGAGGGGCT | 816 |
| QY | 194 | CGCGTTGATTAAGTGTGGGTAAATGCCACCAAGCCGACGATCCATAGTGGT | 253 |
| Db | 815 | CGCGTCTGATTAAGTGTGGGTAAATGCCACCAAGCCGACGATCCATAGTGGT | 756 |
| QY | 254 | TTGAGAGGATGATGACACACACTGGGACTGAGACAGCGGCCACAGCTCTACGGGAGC | 313 |
| Db | 755 | CCGAGAGGATGATGACACACACTGGGACTGAGACAGCGGCCACAGCTCTACGGGAGC | 696 |
| QY | 314 | CAGTGGGAATCTTAGCAATGGGGCAACCTGATCTAGCCATGCGCGTGGTGTGATGA | 373 |
| Db | 695 | CAGTGGGAATTTTCCGCAATGGGGCAACCTGATCTAGCCATGCGCGTGGTGTGATGA | 636 |
| QY | 374 | AGGCTTAAAGTGTAAAGCTCTTTACGCTGGGAAGA--TAATGACGGTACCAGCAGAAG | 431 |
| Db | 635 | AGGCTTAAAGTGTAAAGCTCTTTACGCTGGGAAGA--TAATGACGGTACCAGCAGAAG | 516 |
| QY | 432 | RAGCCCCGGCTAACTCCGTCGACGAGCGCGGTATACGGAGGGGGCTAGCGTTCTCG | 491 |
| Db | 575 | RAGCATCGGCTAACTCTGTCGACGAGCGCGGTATACAGAGGATCAAGGGTTATCGG | 516 |

| | | | |
|----|-----|---|------|
| QY | 492 | GAATTAATGGGCGTAAAGCGCAGCTAGGGGAGTGGAAAGTCAAGAGTGAATCCAGGG | 551 |
| Db | 515 | GAATGATTGGGCGTAAAGCGTCTAGTGGCTTTTAAAGTCCGCGTCAATCCAGGG | 456 |
| QY | 552 | CTCAACCTTGGAACTATCAGTCTGGAGTTCAGAGAGTGGAGTGGTGAAT | 611 |
| Db | 455 | CTCAACCTTGGAACTATCAGTCTGGAGTTCAGAGAGTGGAGTGGTGAAT | 396 |
| QY | 612 | TCGAGTGTAGAGTCAAAATTCAGATATTCGAGAGAACACACAGTGGCGAGCGGCTC | 671 |
| Db | 395 | TTCCGCTGAGAGCGGTGAATGCTAGAGATCGAAGAACACACAGTGGCGAGCGGCTC | 336 |
| QY | 672 | ACTGGCTGCATCTAGCTGAGTGGTGGAAAGCGTGGGAGGAGCAAAAGTATGATACC | 731 |
| Db | 335 | GCTGGCGGACACTGACACTGAGAGACGAAAGCTAGGGAGCGAATGGGATGATACCC | 276 |
| QY | 732 | TGCTAGTCCACGCCGTAACGATGAATGCCAGAG--TCGGCAAGCATGCTTGTGGTGT | 789 |
| Db | 275 | CAGTAGTCTAGCCGTAACGATGATGATGATGATGATGATGATGATGATGATGATG | 216 |
| QY | 790 | CACACCTAACGATTAAAGCATTCGCGCTGGGAGTACGGTTCGCAAGATTAAACTCAA | 849 |
| Db | 215 | TGTAGCTAACGATTAAAGCATTCGCGCTGGGAGTACGGTTCGCAAGATTAAACTCAA | 156 |
| QY | 850 | GAATTGACGGGGCGCGCACACGCGTGGAGCATGTGTTTAAATTCGAAGCAACGCGC | 909 |
| Db | 155 | GAATTGACGGGGCGCGCACACGCGTGGAGCATGTGTTTAAATTCGAAGCAACGCGC | 96 |
| QY | 910 | AACCTTACCAACCTTTGACATGCGCAGACCGCTGGAGAGATTCAGCTTTCTCGTAA | 969 |
| Db | 95 | AACCTTACCAACCTTTGACATGCGCAGACCGCTGGAGAGATTCAGCTTTCTCGTAA | 36 |
| QY | 970 | CCTGCACACAGTGTGCTGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 1004 |
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Search completed: July 28, 2003, 11:41:51
 Job time: 2894 secs